

CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 86; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSMGKEDLIWELL 17
DB 1 VVARSMGKEDLIWELL 17
RESULT 2
ADP30379
ID ADP30379 standard; protein; 200 AA.
XX
AC ADP30379;
XX
DT 01-DEC-2005 (revised)
DT 12-AUG-2004 (first entry)
XX
XX Human secreted protein SEQ ID #3377.
DE
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KM Cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
XX WO2004035732-A2.
XX
PD 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
XX 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.

PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476611P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang WM, Kochakota S, Haisan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX
PS Claim 1; SEQ ID NO 2377; 428bp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytosstatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
CC
CC Revised record issued on 01-DEC-2005 : Sequence description line
CC corrected
XX
SQ Sequence 200 AA;
Query Match 100.0%; Score 86; DB 8; Length 200;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSMGKEDLIWELL 17
DB 124 VVARSMGKEDLIWELL 140

RESULT 3
ADH89432
XX ADH89432 standard; protein; 220 AA.
XX
XX
XX ADH89432;
XX
XX
XX 15-APR-2004 (first entry)
XX
XX Human transferrin fusion protein-related mTF PREX0080 protein SeqID76.
XX
XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytosolic; antibacterial; virucide;
XX anti-parasitic; immunosuppressive; anti-arthritic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection; PREX0080; mTF.
XX
XX Unidentified.
XX
XX US2003226155-A1.
XX
XX 04-DEC-2003.
XX
XX 10-MAR-2003; 2003US-00384060.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Sadeghi H, Prior CP, Turner A;
XX WPI; 2004-022093/02.
XX DR N-PSDB; ADH89431.
XX
XX New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.
XX
XX Example 2; SEQ ID NO 76; 82pp; English.
XX
XX This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC anti-parasitic, immunosuppressive or anti-arthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a protein which was used in the exemplification of
CC the invention.
XX
XX Sequence 220 AA;
XX
XX Query Match 100.0%; Score 86; DB 8; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VVARSMGKEDLIWELL 17
XX |||||||||||||
XX 183 VVARSMGKEDLIWELL 199

RESULT 4
ADL70790
ID ADL70790 standard; protein; 371 AA.

XX ADL70790;
XX
XX 03-JUN-2004 (first entry)
XX
XX
XX Transferrin N-domain protein, SEQ ID 63.
XX
XX
XX Immunosuppressive; Haemostatic; Anti-allergic; Anti-asthmatic;
XX Dermatological; Anti-inflammatory; Antibacterial; Vasculoprotic;
XX Nephroprotective; Neuroprotective; Cytostatic; Cerebroprotective; Vulnery;
XX Anti-parasitism; Neurotropic; Cardiac; Anti-nausea; Anti-atherosclerotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein.
XX
XX Synthetic.
XX
XX WO2004020588-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US026779.
XX
XX 30-AUG-2002; 2002US-0406977P.
XX 10-MAR-2003; 2003US-00384060.
XX 09-JUL-2003; 2003US-0485404P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Prior CP, Turner AJ, Sadeghi H;
XX WPI; 2004-239175/22.
XX DR N-PSDB; ADL70789.
XX
XX Novel library containing several fusion proteins each of which comprises
PT first transferrin polypeptide fused to at least one second peptide,
PT useful for screening for transferrin fusion protein having the particular
PT activity.
XX
XX Example 13; SEQ ID NO 63; 243pp; English.
XX
XX The present invention relates to a library (I) of modified fusion
CC proteins of transferrin (Tf) and therapeutic proteins with increased
CC serum half-life or serum stability. Preferred fusion proteins include
CC those modified so that the Tf moiety exhibits no or reduced
CC glycosylation, iron binding and/or Tf receptor binding. The transferrin
CC fusion proteins are useful for treating, preventing or ameliorating
CC disorders or diseases of endocrine system, nervous system, immune system,
CC respiratory system, cardiovascular system, diseases and/or disorders
CC relating to cell proliferation, and/or diseases or disorders relating to
CC blood. The modified fusion proteins are useful in diagnosis, prognosis,
CC prevention and/or treatment of autoimmune disorders; diseases and
CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
CC and thrombocytopenia); allergic reactions such as asthma, rhinitis and
CC anaphylaxis; IgE-mediated allergic reactions such as allergic asthma,
CC eczema; inflammatory conditions e.g., inflammation associated with
CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel
CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
CC fusion protein is also useful as an adjuvant to enhance antibacterial or
CC antifungal immune responses, anti-parasitic immune responses, etc. The
CC fusion protein is also useful for treating monoclonal gammopathy of
CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytoma,
CC adult respiratory distress syndrome, for stimulating wound repair, for
CC preventing or treating infections of joints, bones, skin, etc. The fusion
CC protein is also useful for treating or preventing thrombosis, myocardial
CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
CC atherosclerosis, etc. In an example from the invention, a system of
CC peptide display for generating peptide sequences uses the N-domain of Tf
CC incorporated into the pIII protein and the insertion of random peptides

CC within the Tf scaffold. The present sequence was used to illustrate this
CC example.

XX Sequence 371 AA;

Query Match 100.0%; Score 86; DB 8; Length 371;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17

DB 274 VVARSWGKEDLIWELL 290

RESULT 5

AAU02980

ID AAU02980 standard; protein; 539 AA.

XX AAU02980;

DT 12-SEP-2001 (first entry)

XX Angiotensin converting enzyme (ACEV) splice variant protein #80.

XX Angiotensin converting enzyme splice variant: ACEV; interleukin 6;
KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KM platelet-derived endothelial cell growth factor; cardiovascular disease;
KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KM vasodilator intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KM myocardial infarction; coronary arterial thrombosis; renal disease;
KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KM noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
KM vascular disorder; asbestosis.

XX Homo sapiens.

XX MO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000MO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX WPI; 2001-336004/35.

XX N-PSDB; AAS06080.

XX Novel alternative splicing variants e.g. variant of angiotensin

XX converting enzyme (ACEV), useful in identifying candidate compounds

XX capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 80; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptide of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasodilator intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such

CC as atherosclerosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

XX Sequence 539 AA;

Query Match 100.0%; Score 86; DB 4; Length 539;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17

DB 143 VVARSWGKEDLIWELL 159

RESULT 6

ABR82321

ID ABR82321 standard; protein; 575 AA.

XX ABR82321;

DT 06-NOV-2003 (first entry)

XX Human metalloprotein (MEPR) polypeptide (id-7509328CD1).

XX MEPR; metalloprotein; anti-HIV; antiallergic; antiinflammatory; human;
KM antineoplastic; antiparkinsonian; nootropic; anticonvulsant; cytostatic;
KM antidiabetic; antidiabetic; immunosuppressive; antithyroid;
KM hepatocellular; dermatological; antidiabetic; nephrotoxic; antitumor;
KM thymomimetic; neuroprotective; osteoprotective; antiallergic; uterine;
KM antiparasitic; antihelminthic; antiparasitic; ophthalmological; vitreous;
KM antineoplastic; haemostatic; antibacterial; protozoacide; fungicide;
KM gene therapy; transgenic.

XX Homo sapiens.

XX MO2003060089-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003MO-US001485.

XX 14-JAN-2002; 2002US-0348769P.

XX 18-JAN-2002; 2002US-0350701P.

XX 10-MAR-2002; 2002US-0366059P.

XX 10-MAY-2002; 2002US-0379907P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW,

XX Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Margulis JP,

XX Tang YT;

XX WPI; 2003-598523/56.

XX N-PSDB; ACF35812.

XX New human metalloproteins and polynucleotides, useful for diagnosing,

XX treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,

XX allergy or anemia), multiple sclerosis, osteoarthritis, cancer or

XX hepatitis.

XX Claim 1; Page 146-148; 153pp; English.

XX The invention relates to novel human metalloproteins (MEPR) and encoding
CC polynucleotides. The human MEPR polypeptides, polynucleotides and
CC modulators are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MEPR, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a ditbp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 643 AA;

Query Match 100.0%; Score 86; DB 8; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWEEL 17
|
Db 251 VVARSMGKEDLIWEEL 267

RESULT 9
ABM83783
ID ABM83783 standard; protein; 645 AA.

XX AC ABM83783;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4032.

XX KM gene therapy; human diagnostic and therapeutic polynucleotide; ditbp.

XX OS Homo sapiens.

XX PN MO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410250P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;
PI Hartshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV;
PI Mooney EM, Deleogene AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kiron ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WPI, 2004-329368/30.

XX DR N-PSDB; ACN42435.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (ditbp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorder, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The ditbp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a ditbp protein of the

CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 645 AA;

Query Match 100.0%; Score 86; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWEEL 17
|
Db 217 VVARSMGKEDLIWEEL 233

RESULT 10
AAU02938
ID AAU02938 standard; protein; 646 AA.

XX AC AAU02938;

XX DT 12-SEP-2001 (first entry)

XX DE Angiotensin converting enzyme (ACEV) splice variant protein #38.

XX KM Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
XX platelet-derived endothelial cell growth factor; cardiovascular disease;
XX cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
XX vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
XX myocardial infarction; coronary arterial thrombosis; renal disease;
XX diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
XX multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
XX vascular disorder; asbestosis.

XX OS Homo sapiens.

XX PN MO200136632-A2.

XX PD 25-MAY-2001.

XX PF 17-NOV-2000; 2000WO-IL000766.

XX PR 17-NOV-1999; 99IL-00132978.

XX PR 10-DEC-1999; 99IL-00133455.

XX PA (COMP-) COMPUGEN LTD.

XX PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX WPI, 2001-336004/35.

XX DR N-PSDB; AAS06038.

XX PT Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 38; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
XX (ACEV) polypeptide. The polypeptides of the invention include variants of
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
XX polypeptide receptor 2. The polypeptides and their associated nucleic
XX acids are useful for identification of variant sequences and detection of
XX candidate compounds capable of binding to the molecules. The sequences of
XX the invention can be used in the treatment and diagnosis of various
XX disorders including cardiovascular diseases such as arteriosclerosis,
XX myocardial infarction and coronary arterial thrombosis, renal diseases
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX immune disorders such as immune complex nephritis, multiple sclerosis,

CC cancer, sarcoidosis, nonarchoidotic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis
XX

SO Sequence 646 AA;

Query Match 100.0%; Score 86; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVARSMGKEDLIWELL 17
|||
Db 270 VVARSMGKEDLIWELL 286

RESULT 11

AAU02937
ID AAU02937 standard; protein: 665 AA.

XX AAU02937;

DT 12-SEP-2001 (first entry)

XX Angiotensin converting enzyme (ACEV) splice variant protein #37.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KM platelet-derived endothelial cell growth factor; cardiovascular disease;
KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KM vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KM myocardial infarction; coronary arterial thrombosis; renal disease;
KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KM nonarchoidotic pulmonary granulomatous disease; endothelial abnormality;
KM vascular disorder; asbestosis.

XX Homo sapiens.

OS WO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000MO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMFUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX WPI: 2001-336004/35.

XX N-PSDB; AAS06037.

XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 37; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,

CC cancer, sarcoidosis, nonarchoidotic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis
XX

SO Sequence 665 AA;

Query Match 100.0%; Score 86; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVARSMGKEDLIWELL 17
|||
Db 270 VVARSMGKEDLIWELL 286

RESULT 12

ABP72820
ID ABP72820 standard; protein: 679 AA.

XX ABP72820;

DT 11-AUG-2003 (first entry)

XX Human transferrin (mature polypeptide).

XX Human; transferrin; neuroprotective; cerebroprotective; vasotropic;
KM antiparkinsonian; nootropic; anti-HIV; antiasthmatic; anti-allergic;
KM cyostatic; immunosuppressive; antiatherosclerotic; cardiant;
KM gynaecological; immunostimulant; anaemic; haemostatic;
KM antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
KM fungicide; hepatotropic; antirheumatic; antiarthritic; antiscour;
KM tranquilizer; vulnerary; antidiabetic; nephrotropic; antipyretic;
KM gastrointestinal; gene therapy; transgenic animal.

XX Homo sapiens.

OS

XX Key

XX Binding-site

XX Region

XX Binding-site

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XX Binding-site

XX Binding-site

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XX Binding-site

XX Binding-site

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FT Binding-site 459 /note= "Carbonate ion binding site"
FT Binding-site 514 /note= "Iron binding site"
FT Binding-site 517 /note= "Iron binding site"
FT Binding-site 581 /note= "Iron binding site"
FT Region 582 /note= "Hinge region"
FT Binding-site 585 /note= "Iron binding site"
FT Modified-site 611 /note= "N-glycosylated"
FT Region 652 /note= "Hinge region"
FT /note= "Hinge region"
XX WO2003020746-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027637.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX
XX (BIOREXIS PHARM CORP.
XX Prior CP;
XX WPI; 2003-332916/31.
XX
XX New fusion protein, useful in the diagnosis and treatment of diseases or
XX disorders relating to the respiratory, cardiovascular and digestive
XX systems, comprises a transferrin protein fused to a therapeutic protein.
XX
XX Disclosure; Page 280-281; 299pp; English.
XX
XX The present sequence is the protein sequence of human transferrin (Tf),
XX minus the signal peptide. The invention relates to modified Tf fusion
XX proteins comprising at least one therapeutic protein, polypeptide or
XX peptide, in which the Tf portion is engineered to extend the serum half-
XX life or bioavailability of the molecule. The modified Tf fusion protein
XX preferably comprises a human Tf moiety that has been modified to reduce
XX or prevent glycosylation, iron binding and/or transferrin receptor
XX binding, having at least one amino acid substitution, deletion or
XX addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-
XX 188, Lys-206, His-207, His-249, Asp-392, Tyr-426, Tyr-514, Tyr-517, His-
XX 585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and
XX Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611
XX (all claimed). Nucleic acids encoding such fusion proteins, vectors, host
XX cells and transgenic animals which produce the fusion protein in their
XX serum or milk are also claimed. The modified fusion protein is useful for
XX treating a disease or disease symptom, or for delivering a therapeutic
XX agent complexed to the ferric iron of transferrin to the inside of a cell
XX or across the blood-brain barrier. The modified fusion protein, or a
XX nucleic acid encoding it, can be used in the diagnosis, prognosis,
XX prevention and/or treatment of diseases and/or disorders of the
XX endocrine, nervous, immune, respiratory, cardiovascular, reproductive and
XX digestive systems, diseases and/or disorders relating to the blood or to
XX cell proliferation, inflammatory conditions, and to treat viral, fungal,
XX bacterial or parasitic infection
XX
XX Sequence 679 AA:
XX
XX Query Match 100.0%; Score 86; DB 6; Length 679;
XX Best Local Similarity 100.0%; Pred. No. 2e-05;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VVARSMGKEDLIWELL 17
XX |||||
XX Db 251 VVARSMGKEDLIWELL 267
XX
XX RESULT 13

```

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ADH89360
ID ADH89360 standard; protein; 679 AA.
XX
XX ADH89360;
XX
XX 15-APR-2004 (first entry)
XX
XX Human transferrin protein mature amino acid sequence.
XX
XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytosolic; antibacterial; virucide;
XX antiparasitic; immunosuppressive; antiarthritic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection; human.
XX
XX Homo sapiens.
XX
XX US2003226155-A1.
XX
XX 04-DEC-2003.
XX
XX 10-MAR-2003; 2003US-00384060.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOREXIS PHARM CORP.
XX
XX Sadeghi H, Prior CP, Turner A;
XX WPI; 2004-022093/02.
XX
XX N-PSDB; ADH89358.
XX
XX New fusion protein comprising a transferrin protein exhibiting reduced
XX glycosylation fused to at least one antibody variable region, useful for
XX preparing a composition for treating e.g., septic shock, neoplasm or
XX autoimmune disease.
XX
XX Disclosure; SEQ ID NO 3; 82pp; English.
XX
XX This invention relates to a novel fusion protein which comprises a
XX transferrin protein exhibiting reduced glycosylation fused to at least
XX one antibody variable region. The invention may be useful for the
XX development of compounds with cytosolic, antibacterial, virucide,
XX antiparasitic, immunosuppressive or antiarthritic activity. In addition,
XX the sequences disclosed may be useful for gene therapy. The fusion
XX protein is useful for preparing a composition for treating a disease or
XX disease symptom in a patient for example septic shock, endotoxic shock,
XX cachexia syndromes associated with bacterial, viral or parasitic
XX infections, neoplasm, autoimmune disease, arthritis or adverse effects
XX associated with treatment for preventing graft rejection. The present
XX sequence is that of the mature human transferrin protein which is related
XX to the invention.
XX
XX Sequence 679 AA:
XX
XX Query Match 100.0%; Score 86; DB 8; Length 679;
XX Best Local Similarity 100.0%; Pred. No. 2e-05;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VVARSMGKEDLIWELL 17
XX |||||
XX Db 251 VVARSMGKEDLIWELL 267
XX
XX RESULT 14
XX ADK15869
XX ID ADK15869 standard; protein; 679 AA.
XX
XX ADK15869;
XX

```

```

XX 06-MAY-2004 (first entry)
XX Mature human transferrin (Tf) protein.
DE fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
XX glucagon-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
KM T-20; soluble toxin receptor; epitope tagging; human.
XX Homo sapiens.
OS US2003221201-A1.
XX
XX 27-NOV-2003.
XX
XX 04-MAR-2003; 2003US-00378094.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Prior CP, Lai C, Sadeghi H, Turner A,
XX WPI; 2004-010899/01.
XX
XX New fusion protein comprising a modified transferrin (Tf) protein fused
XX to a therapeutic protein or peptide, useful for epitope tagging.
XX
XX Example 5; SEQ ID NO 3; 70pp; English.
XX
XX The invention comprises a fusion protein that contains a modified
XX transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.
XX beta-interferon - IFN, glucagons-like peptide - GLP-1, erythropoietin
XX mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
XX protein of the invention is useful for epitope tagging. The present amino
XX acid sequence represents the mature human Tf protein.
XX
XX Sequence 679 AA;
SQ
Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267
RESULT 15
ADL70732
ID ADL70732 standard; protein; 679 AA.
XX
XX ADL70732;
AC
XX
XX 03-JUN-2004 (first entry)
XX
XX Human transferrin, Tf, mature protein SEQ ID 3.
XX
XX Immunosuppressive; Haemostatic; Antiallergic; Antiaesthetic;
XX Dermatological; Antiinflammatory; Antibacterial; Vasotrophic;
XX Nephroprotective; Cytostatic; Cerebroprotective; Vulnerary;
XX Antiparkinsonian; Neurotropic; Cardiant; Antianemic; Antithrombotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein; human.
XX
XX Homo sapiens.
XX
XX WO2004020588-A2.
XX
XX 11-MAR-2004.
XX

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XX 28-AUG-2003; 2003WO-US026779.
XX
XX 30-AUG-2002; 2002US-0406977P.
XX 10-MAR-2003; 2003US-00384060.
XX 09-JUL-2003; 2003US-0485404P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Prior CP, Turner AJ, Sadeghi H;
XX WPI; 2004-239175/22.
XX DR N-PSDB; ADL70730.
XX
XX Novel library containing several fusion proteins each of which comprises
XX first transferrin polypeptide fused to at least one second peptide,
XX useful for screening for transferrin fusion protein having the particular
XX activity.
XX
XX Claim 44; SEQ ID NO 3; 243pp; English.
XX
XX The present invention relates to a library (I) of modified fusion
XX proteins of transferrin (Tf) and therapeutic proteins with increased
XX serum half-life or serum stability. Preferred fusion proteins include
XX those modified so that the Tf moiety exhibits no or reduced
XX glycosylation, iron binding and/or Tf receptor binding. The transferrin
XX fusion proteins are useful for treating, preventing or ameliorating
XX disorders or diseases of endocrine system, nervous system, immune system,
XX respiratory system, cardiovascular system, diseases and/or disorders
XX relating to cell proliferation, and/or diseases or disorders relating to
XX blood. The modified fusion proteins are useful in diagnosis, prognosis,
XX prevention and/or treatment of autoimmune disorders; diseases and
XX disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
XX and thrombocytopenia); allergic reactions such as allergic asthma,
XX anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
XX eczema; inflammatory conditions e.g., inflammation associated with
XX infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
XX hepatitis, Crohn's disease, multiple sclerosis, respiratory disorders
XX (asthma and allergy), gastrointestinal disorders (inflammatory bowel
XX disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
XX (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
XX disorders such as Parkinson's disease, Alzheimer's disease), etc. The
XX fusion protein is also useful as an adjuvant to enhance antibacterial or
XX antifungal immune responses, antiparasitic immune responses, etc. The
XX fusion protein is also useful for treating monoclonal gammopathy of
XX undetermined significance (MGUS), Waldenström's disease, plasmacytomas,
XX adult respiratory distress syndrome, for stimulating wound repair, for
XX preventing or treating infections of joints, bones, skin, etc. The fusion
XX protein is also useful for treating or preventing thrombosis, myocardial
XX infarction, cancers, thrombocytopenia, sickle cell anaemia,
XX glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
XX atherosclerosis, etc. The present sequence is human Tf mature protein,
XX used to make the modified Tf fusion proteins of the invention.
XX
XX Sequence 679 AA;
SQ
Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267
Search completed: June 13, 2006, 03:58:16
Job time : 110 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:18:14 ; Search time 17.25 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86

Sequence: 1 VVARSNGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gaepct 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 80.*
2: p1r1.*
3: p1r2.*
4: p1r3.*
5: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	86	100.0	698 1	TFHUP
2	75	87.2	694 1	TFRBP
3	75	87.2	704 2	147228
4	71	82.6	708 1	TFBOL
5	70	81.4	708 2	JC2323
6	68	79.1	706 2	S33761
7	66	76.7	695 2	S49163
8	66	76.7	711 1	TFHUP
9	65	75.6	696 1	S01384
10	65	75.6	703 2	A45543
11	55	64.0	707 1	A28438
12	52	60.5	434 2	A28446
13	49.5	57.6	459 2	A75097
14	47.5	55.2	510 2	G72464
15	45	52.3	2958 2	S64921
16	44	51.2	386 2	A70740
17	44	51.2	885 2	AG3350
18	43	50.0	210 1	27BP79
19	43	50.0	439 2	T49907
20	43	50.0	2140 2	T18543
21	42	48.8	164 2	S20525
22	42	48.8	882 2	PC1231
23	42	48.8	970 2	I78842
24	42	48.8	995 2	A56599
25	41	47.7	99 2	A22848
26	41	47.7	324 2	C83695
27	41	47.7	326 2	S75131
28	41	47.7	346 2	F75377
29	41	47.7	451 2	F75131

30	41	47.7	452	2	E71154	hypothetical prote
31	41	47.7	559	2	A99237	hypothetical prote
32	41	47.7	559	2	JC5616	group II chaperoni
33	41	47.7	560	2	S59859	riboseome alpha
34	41	47.7	853	2	A95269	probable sensory t
35	41	47.7	1502	2	T42216	multidrug resistanc
36	41	47.7	1677	2	T46095	hypothetical prote
37	41	47.7	1938	1	S06005	myosin alpha heavy
38	40.5	47.1	201	2	S75047	dyga protein - Syn
39	40	46.5	98	2	T14691	hypothetical prote
40	40	46.5	103	2	A10259	hypothetical phage
41	40	46.5	136	2	T15031	hypothetical prote
42	40	46.5	169	2	AD1293	hypothetical prote
43	40	46.5	307	2	D36868	copd homolog - Xan
44	40	46.5	374	2	D81937	probable ribosomal
45	40	46.5	403	2	H83477	conserved hypochet

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor [validated] - human
N/Alternate names: siderophilin
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1982 #sequence, revision 30-Sep-1993 #text change 09-Jul-2004
C/Accession: A20981; A92417; A24044; A29090; A32739; I51959; I63133; I54011; I68160; A033
R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A/Title: Human transferrin: cDNA characterization and chromosomal localization.
A/Reference number: A20981; MUID:84194084; PMID:6585826
A/Contents: variant C
A/Accession: A20981
A/Molecule type: mRNA
A/Residues: 1-698 <YAN>
A/Cross-references: UNIPROT:P02787; UNIPARC:UPI000002F089; EMBL:M12530; NID:G339452; PIDN
A/Note: The authors translated the codon CAA for residue 203 as Glu
R/McGillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Linbeck-Zins, J.; Brew,
J. Biol. Chem. 258, 3543-3553, 1983
A/Title: The primary structure of human serum transferrin. The structures of seven cyanog
A/Reference number: A92417; MUID:83160878; PMID:6833213
A/Accession: A92417
A/Molecule type: protein
A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-5
A/Cross-references: UNIPARC:UPI0000174483
A/Note: the sequence shown is the predominant electrophoretic genetic variant (C or T/C)
R/Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A/Title: Organization of the human transferrin gene: direct evidence that it originated b
A/Reference number: A94044; MUID:85216459; PMID:3858812
A/Accession: A94044
A/Molecule type: DNA
A/Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A/Cross-references: UNIPARC:UPI0000174484; EMBL:M11361
R/Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A/Title: The human transferrin gene: 5' region contains conserved sequences which match t
A/Reference number: A29090; MUID:87192006; PMID:33106157
A/Accession: A29090
A/Molecule type: DNA
A/Residues: 1-72, 291-300 <ADR>
A/Cross-references: UNIPARC:UPI000016B0AC; UNIPARC:UPI000016B0AD; EMBL:M15673
R/Uan, G.; Fraim, M.; Park, I.; Besmond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; Kai
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A/Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A/Reference number: A32739; MUID:84153910; PMID:6322780
A/Accession: A32739
A/Molecule type: mRNA
A/Residues: 422-690, 'G', 692-698 <UZA>
A/Cross-references: UNIPARC:UPI000016B0AB; EMBL:M1525; NID:G339468; PIDN:AAA61142.1; PIR
R/McGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Linbeck-Zins, J.; Brew, H

Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982
 A>Title: The complete amino acid sequence of human serum transferrin.
 A/Reference number: A93911; MUID:8222166; PMID:6953407
 A/Content: annotation; disulfide bonds
 R/Hershbeger, C.L.; Larson, J.L.; Arnold, B.; Roseck, P.R.
 Ann. N. Y. Acad. Sci. 646, 140-154, 1991
 A>Title: A cloned gene for human transferrin.
 A/Reference number: 151959; MUID:92231399; PMID:1809186
 A/Accession: 151959
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-698 <RES>
 A/Cross-references: UNIPARC:UPI00002F089; GB:S95936; NID:g248647; PIDN:AMB22049.1; PID:R/Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtelotte, W.W.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
 A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
 A/Reference number: 148174; MUID:8936721; PMID:2780570
 A/Accession: 163133
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 636-696 <RE2>
 A/Cross-references: UNIPARC:UPI000016B13C; GB:M26641; NID:g339988; PIDN:AAA61233.1; PID:R/Schaeffer, E.; Lucero, M.A.; Jeltsch, J.M.; Py, M.C.; Levin, M.J.; Chamoun, P.; Cohen, Gene 56, 109-116, 1987
 A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
 A/Reference number: 154011; MUID:88056305; PMID:3678832
 A/Accession: 154011
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-72 <RE3>
 A/Cross-references: UNIPARC:UPI000016B0AC; GB:M17611; NID:g339480; PIDN:AAA61147.1; PID:A/Accession: 168160
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 564-698 <RE4>
 A/Cross-references: UNIPARC:UPI000016B0AE; GB:M17614; NID:g339483; PIDN:AAA61148.1; PID:A/Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
 C/Genetic: 8
 A/Genes: GDB:TF
 A/Cross-references: GDB:120432; OMIM:190000
 A/Map position: 3q21-3q21
 A/Intons: 15/1; 72/3; 119/1; 168/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
 C/Function: 1
 A/Description: binds iron for delivery into cells
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-698/Product: transferrin #status experimental <MAT>
 F:20-350/Domain: transferrin repeat homology <TRH1>
 F:356-686/Domain: transferrin repeat homology <TRH2>
 F:28-67;36-58;137-213;156-350;177-193;180-196;190-198;246-260;358-615;364-396;374-387;42
 F:432;630/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 86; DB 1; Length 698;
 Best Local Similarity 100.0%; Pred. No. 1 6e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
 DB 270 VVARSMGKEDLIWELL 286

RESULT 2

TFRBP
 transferrin precursor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text change 22-Jun-1999
 C/Accession: S16246; A61233; C61573; S00335; S02699; A26504; S1853
 R/Bantfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umelae, T.M.; Woodworth, R.
 Biochim. Biophys. Acta 1089, 262-265, 1991
 A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
 A/Reference number: S16246; MUID:91274362; PMID:2054387
 A/Accession: S16246

A/Molecule type: mRNA
 A/Residues: 1-694 <BAN>
 A/Cross-references: UNIPARC:UPI000016C5CB; EMBL:X58533; NID:g1750; PIDN:CAA41424.1; PID:R/Pierpaoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
 Cell. Immunol. 134, 225-234, 1991
 A>Title: Iron carrier proteins facilitate engorgement of allogeneic bone marrow and endu
 A/Reference number: A61239; MUID:9191504; PMID:2013104
 A/Accession: A61239
 A/Molecule type: protein
 A/Residues: 19-36 <PIE>
 A/Cross-references: UNIPARC:UPI00001744A6
 R/Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
 A/Reference number: A61573; MUID:91293379; PMID:2065820
 A/Accession: C61573
 A/Molecule type: protein
 A/Residues: 19-26; 'X', 28-36; 'X', 38-53 <CHU>
 A/Cross-references: UNIPARC:UPI00001744A7
 R/Godovac-Zimmermann, J.
 Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
 A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transfe
 A/Reference number: S00335; MUID:88209278; PMID:3365331
 A/Accession: S00335
 A/Molecule type: protein
 A/Residues: 19-45; 'S', 47-48; 'Y', 50 <GOD>
 A/Cross-references: UNIPARC:UPI00001744A8
 R/Evans, R.W.; Aitken, A.; Patel, K.J.
 FEBS Lett. 239, 39-42, 1988
 A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
 A/Reference number: S02694; MUID:89005676; PMID:3169252
 A/Accession: S02694
 A/Molecule type: protein
 A/Residues: 482-515; 'V', 517-544 <EVA>
 A/Cross-references: UNIPARC:UPI00001744A9
 A/Note: 516-Ile was also found
 R/Heapy, S.; Williams, J.
 Biochem. J. 205, 611-617, 1982
 A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-
 A/Reference number: A26504; MUID:83074540; PMID:6816218
 A/Accession: A26504
 A/Molecule type: protein
 A/Residues: 19-24; 'N', 26; 'X', 28-29; 'S', <HEA>
 A/Cross-references: UNIPARC:UPI00001744AA
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-694/Product: transferrin #status experimental <MAT>
 F:19-349/Domain: transferrin repeat homology <TRH1>
 F:355-682/Domain: transferrin repeat homology <TRH2>
 F:27-66;37-57;136-212;155-349;176-192;179-195;189-197;245-259;357-611;363-395;373-386;42
 F:508/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 87.2%; Score 75; DB 1; Length 694;
 Best Local Similarity 88.2%; Pred. No. 0.00012;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
 DB 269 VVARSMGKEDLIWELL 285

RESULT 3

I47228
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text change 09-Jul-2004
 C/Accession: I47228
 R/Roun, E.D.; Fierke, C.A.
 Biochemistry 31, 12336-12342, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from porc
 A/Reference number: I47228; MUID:93099129; PMID:1463741
 A/Accession: I47228

A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-704 <ROU>
 A:Cross-references: UNIPROT:Q29545; UNIPARC:UPI000012P142; EMBL:U36916; NID:g1016329; P1
 C:Genetics: pICA
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication
 F:20-350/Domain: transferrin repeat homology <TRH1>
 Query Match 87.2%; Score 75; DB 2; Length 704;
 Best Local Similarity 88.2%; Pred. No. 0.00013;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VVARSMGKEDLIWELL 17
 Db 270 VVARSVGKEDLIWELL 286
 RESULT 4
 laccotransferrin precursor - bovine
 N:Alternate names: lactoferrin
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 09-Jul-2004
 C:Accession: I45919; S14674; S14110; S18517; S13097; S18518; S13881; P10148; S21
 R:Yang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 FASEB J. 6, 233, 1991
 A:Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein frc
 A:Reference number: I45919
 A:Accession: I45919
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-708 <TSA>
 A:Cross-references: UNIPROT:P24627; UNIPARC:UPI000013J377; GB:L08604; NID:g163269; PIDN:
 R:Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A:Reference number: S14674
 A:Accession: S14674
 A:Molecule type: mRNA
 A:Residues: 1-144,'V',146-163,'P',166-339,'A',341-438,'Y',440-513,'R',515-708 <PI1>
 A:Cross-references: UNIPARC:UPI00001C335; EMBL:X57084; NID:9505; PIDN:CA40366.1; PID:
 R:Pierce, A.; Colavizza, D.; Benalissa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A:Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A:Reference number: S14110; NUID:91160550; PMID:2001696
 A:Accession: S14110
 A:Molecule type: mRNA
 A:Residues: 3-144,'V',146-339,'A',341-438,'Y',440-513,'R',515-708 <PI2>
 A:Cross-references: UNIPARC:UPI000017448B; EMBL:X57084
 A:Accession: S18517
 A:Molecule type: protein
 A:Residues: 20-35;88-114;148-163,'P',166-178,'V',183-190;205-212;230-239;304-339;59
 A:Cross-references: UNIPARC:UPI000017448C; UNIPARC:UPI000017448D; UNIPARC:UPI000017448E;
 493; UNIPARC:UPI0000174494
 R:Goodman, R.E.; Schanbacher, F.T.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A:Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary glar
 A:Reference number: J70595; NUID:92028986; PMID:1718281
 A:Accession: J70595
 A:Molecule type: mRNA
 A:Residues: 1-65,'P',68-296,'S',298-339,'A',341-708 <GOO>
 A:Cross-references: UNIPARC:UPI0000174495; GB:M63502
 A:Title: The authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
 R:Mead, P.E.; Tweedle, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A:Title: CDNA and protein sequence of bovine lactoferrin.
 A:Reference number: S13097; NUID:91088328; PMID:2263492
 A:Accession: S13097
 A:Molecule type: mRNA
 A:Residues: 28-33,'DS',36-38,'P',40-708 <MEA>
 A:Cross-references: UNIPARC:UPI0000174496; EMBL:X54801
 A:Accession: S18518

A:Molecule type: protein
 A:Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586,587-589;598-619
 A:Cross-references: UNIPARC:UPI0000174493; UNIPARC:UPI0000174497; UNIPARC:UPI0000174498;
 49D; UNIPARC:UPI000017449E
 R:Mead, P.E.
 submitted to the EMBL Data Library, October 1990
 A:Reference number: S13881
 A:Accession: S13881
 A:Molecule type: mRNA
 A:Residues: 28-38,'P',40-86,'C',88-708 <ME3>
 A:Cross-references: UNIPARC:UPI000017449F; EMBL:X54801
 R:Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A:Title: Purification and characterization of bovine lactoferrin from secretions of the
 A:Reference number: P10148; NUID:90031466; PMID:2805645
 A:Accession: P10148
 A:Molecule type: protein
 A:Residues: 20-27,'X',29-37,'X',39-54,'X',56-59 <REJ>
 A:Cross-references: UNIPARC:UPI00001744A0
 R:Belamy, W.; Takase, M.; Yamauchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A:Title: Identification of the bactericidal domain of lactoferrin.
 A:Reference number: S21756; NUID:92287941; PMID:1599934
 A:Accession: S21756
 A:Molecule type: protein
 A:Residues: 36-60 <BEL>
 A:Cross-references: UNIPARC:UPI0000475A8
 R:Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A:Title: Separation and characterization of the C-terminal half molecule of bovine lacto
 A:Reference number: A56659; NUID:93253156; PMID:846845
 A:Accession: A56659
 A:Molecule type: protein
 A:Residues: 20-25;302-308;359-366,'X',368-376,'X',378 <SHI>
 A:Cross-references: UNIPARC:UPI00001744A1; UNIPARC:UPI00001744A2; UNIPARC:UPI00001744A3
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-708/Product: lactotransferrin #status experimental <MAT>
 F:20-355/Domain: transferrin repeat homology <TRH1>
 F:36-60/Region: antimicrobial
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:82-64;134-217;176-192;179-200;189-202;250-264;367-399;377-390;424-703;444-666;476-551,
 F:38-55/Dissulfide bonds: #status predicted
 F:79,111,211,272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:140/Binding site: carbonate (Arg) #status experimental
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:414,452,545,614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:482/Binding site: carbonate (Arg) #status experimental
 Query Match 82.6%; Score 71; DB 1; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.00061;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VVARSMGKEDLIWELL 17
 Db 274 VVARSVGKEDLIWELL 290
 RESULT 5
 JUC223
 lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JUC223
 R:Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A:Reference number: JUC223; NUID:94380047; PMID:8093048
 A:Accession: JUC223
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 A:Cross-references: UNIPARC:UPI0000177C50

C:Superfamily: transferrin; transferrin repeat homology

C/Keyword: duplication; glycoprotein

F:559-696/Domain: transferrin repeat homology <TRH>

F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 81.4%; Score 70; DB 2; Length 708;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 274 VVARSDVGKEDLIWELL 290

RESULT 6

transferrin precursor - horse

N:Alternate names: growth-promoting factor

C/Species: Equus caballus (domestic horse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S33761; S02145

R/Carpenter, M.A.; Broad, T.E.

Biochim. Biophys. Acta 1173, 230-232, 1993

A>Title: The cDNA sequence of horse transferrin.

A/Reference number: S33761; MUID:93277958; PMID:8504171

A/Accession: S33761

A/Molecule type: mRNA

A/Residues: 1-706 <CR>

A/Cross-references: UNIPROT:P27425; UNIPARC:UPI0000137370; EMBL:M69020; NID:g164242; PIR

A/Experimental source: liver; developmental stage adult

R/Oshinari, K.; Yuasa, K.; Iga, F.; Mimura, A.

Biochim. Biophys. Acta 1010, 28-34, 1989

A>Title: A growth-promoting factor for human myeloid leukemia cells from horse serum id

A/Reference number: S02145; MUID:89076897; PMID:2909248

A/Accession: S02145

A/Molecule type: protein

A/Residues: 20-35, 'X', '37', 'X', '39-40', 'X', '43-44' <YOS>

A/Cross-references: UNIPARC:UPI0000177C56

C/Complex: monomer

C/Superfamily: transferrin; transferrin repeat homology

C/Keyword: duplication; glycoprotein; iron transport; metal binding; plasma

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-706/Product: transferrin #status experimental <MNT>

F:358-694/Domain: transferrin repeat homology <TRH>

F:26-64,35-55,134-215,174-190,177-198,187-200,248-262,360-623,366-398,376-389,423-701,44

Query Match

Best Local Similarity 79.1%; Score 68; DB 2; Length 706;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 272 VVARSDVGKEDLIWELL 288

RESULT 7

transferrin precursor - rat

N:Alternate names: lung-derived growth factor; siderophilin

C/Species: Rattus norvegicus (Norway rat)

C/Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C/Accession: S49163; S54980; A10014; A14679; A53289; A30512; I52203

R/Schirra, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus

submitted to the EMBL Data Library, January 1994

A/Description: Rat mammary gland transferrin; glycan structure, nucleotide sequence and

A/Reference number: S49163

A/Accession: S49163

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-695 <RSC>

A/Cross-references: UNIPROT:P12346; UNIPROT:O63602; UNIPARC:UPI0000167A8E; EMBL:X77158;

R/Schirra, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus

Biochem. J. 307, 47-55, 1995

A>Title: Rat mammary-gland transferrin; nucleotide sequence, phylogenetic analysis and g]

A/Reference number: S54980; MUID:95234054; PMID:7717992

A/Accession: S54980

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-695 <RSC>

A/Cross-references: UNIPARC:UPI0000167A8E; EMBL:X77158; NID:9510195; PIR:CA54403.1; PIR

R/Hugenvik, J.I.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.

Endocrinology 120, 332-340, 1987

A>Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulatic

A/Reference number: A30014; MUID:87053639; PMID:3023031

A/Accession: A30014

A/Molecule type: mRNA

A/Residues: 518-687, 'D', '689-693', 'TA', '695' <HUG>

A/Cross-references: UNIPARC:UPI0000170B4C; GB:M27966; NID:g207439; PIR:AAA42267.1; PIR

R/Schreibler, G.; Dryburgh, H.; Milnership, A.; Matsuda, Y.; Inglis, A.; Phillips, J.; Edw

J. Biol. Chem. 254, 12013-12019, 1979

A>Title: The synthesis and secretion of rat transferrin.

A/Reference number: A14679; MUID:80049855; PMID:500689

A/Accession: A14679

A/Molecule type: protein

A/Residues: 20-47 <SCH>

A/Cross-references: UNIPARC:UPI0000177C51

R/Cavanaugh, P.G.; Nicolson, G.L.

J. Cell. Biochem. 47, 261-271, 1991

A>Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tunc

A/Reference number: A53289; MUID:92165927; PMID:1791188

A/Accession: A53289

A/Status: preliminary

A/Molecule type: protein

A/Residues: 89, 'Y', '91', 'A', '93-99', 'V', '101-102', 'N', '233', 'AN', '236-243', '401-406', 'N', '408' <CAV>

A/Cross-references: UNIPARC:UPI000006F28; UNIPARC:UPI00000E76D; UNIPARC:UPI00000E7E7F

A/Experimental source: lung after extraction from NCBI backbone

A>Note: Sequence modified after extraction from NCBI backbone (NCBI:P:86115, NCBI:P:86116, NCBI:P:86114)

A/Note: Sequence extracted from NCBI backbone (NCBI:P:86115, NCBI:P:86116, NCBI:P:86114)

R/Purves, L.R.; Purves, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.

Biochim. Biophys. Acta 966, 318-327, 1998

A>Title: Properties of the transferrin associated with rat intestinal mucosa.

A/Reference number: A30512; MUID:88327006; PMID:304665

A/Accession: A30512

A/Molecule type: protein

A/Residues: 20-30, '639-643', 'KD', '646', 'LKAD', 'PUB' <PUB>

A/Cross-references: UNIPARC:UPI0000177C52; UNIPARC:UPI0000177C53

R/Aldred, A.R.; Howlett, G.J.; Schreiber, G.

Biochem. Biophys. Res. Commun. 122, 960-965, 1984

A>Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bacter

A/Reference number: I52203; MUID:84307580; PMID:6236811

A/Accession: I52203

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 7-25, 'X', '27-56', 'A', '58-64', '267-295' <RES>

A/Cross-references: UNIPARC:UPI000005C48; GB:M26113; NID:g207437; PIR:AAA42266.1; PIR

C/Genetics:

A/Gene: TF

C/Superfamily: transferrin; transferrin repeat homology

C/Keywords: duplication

F:20-348/Domain: transferrin repeat homology <TRH>

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
 R:Cho, Y.
 Submitted to the EMBL Data Library, March 1994
 A:Reference number: G06820
 A:Accession: G01394
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-711 <CHO>
 A:Cross-references: UNIPARC:UPI000013737C; EMBL:U07643; NID:g467236; PIDN:AA60324.1; PI
 R:Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
 Nucleic Acids Res. 18, 5288, 1990
 A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.
 A:Reference number: S11228; MUID:90384839; PMID:2402455
 A:Accession: S11228
 A:Molecule type: mRNA
 A:Residues: 1-148; 'T', 150-422; 'C', 424-711 <REV>
 A:Cross-references: UNIPARC:UPI000015C582; EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID
 R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
 Mol. Endocrinol. 6, 1969-1981, 1992
 A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin
 A:Reference number: A45401; MUID:93125571; PMID:1480183
 A:Accession: A45401
 A:Molecule type: DNA
 A:Residues: 1-15 <TEN>
 A:Cross-references: UNIPARC:UPI0000004DD; GB:S52659; NID:g263311; PIDN:AA624877.1; PID
 A:Experimental source: Placenta
 A:Note: Sequence extracted from NCBI backbone (NCBI:P122202)
 R:Powell, M.J.; Ogden, J.E.
 Nucleic Acids Res. 18, 4013, 1990
 A:Title: Nucleotide sequence of human lactoferrin cDNA
 A:Reference number: S10324; MUID:90326549; PMID:2374734
 A:Accession: S10324
 A:Molecule type: mRNA
 A:Residues: 3-711 <POW>
 A:Cross-references: UNIPARC:UPI000016AC28; EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID
 R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
 Biochem. J. 276, 349-355, 1991
 A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
 A:Reference number: S15853; MUID:91264786; PMID:2049066
 A:Accession: S15853
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 20-31 <ST1>
 A:Cross-references: UNIPARC:UPI0000174487
 A:Accession: S20841
 A:Molecule type: protein
 A:Residues: 20-28; 'X', 30-31 <ST2>
 R:Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
 A:Reference number: S07160; MUID:88001031; PMID:3477300
 A:Accession: S07160
 A:Molecule type: mRNA
 A:Residues: 436-487; 'A', 489-711 <RAD>
 A:Cross-references: UNIPARC:UPI000016ABE2; EMBL:M18642; NID:g186915; PIDN:AAA6665.1; PI
 R:Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocy
 A:Reference number: A61169; MUID:91235214; PMID:1674448
 A:Accession: A61169
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 3-701; 'SWKPVN' <PAN>
 A:Cross-references: UNIPARC:UPI000014B632
 A:Experimental source: normal breast tissue
 R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A:Title: Human lactoferrin: amino acid sequence and structural comparisons with oth
 A:Reference number: A31000; MUID:85076667; PMID:6510420
 A:Accession: A31000
 A:Molecule type: protein
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4

A:Cross-references: UNIPARC:UPI0000174489
 A:Note: this is the final paper in a series
 R:Houen, G.; Hoegalli, E.V.; Barkholt, V.; Nørskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affi
 A:Reference number: S74119; MUID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: protein
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A:Cross-references: UNIPARC:UPI000017448A
 A:Experimental source: neutrophil granulocytes
 C:Genetics:
 A:Gene: GDB:UTR
 A:Cross-references: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/Domains: signal sequence #status predicted <SIG>
 F:20-711/Product: lactotransferrin #status experimental <MAT>
 F:21-356/Domains: transferrin repeat homology <TRH1>
 F:360-659/Domains: transferrin repeat homology <TRH2>
 F:29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
 F:157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 76.7%; Score 66; DB 1; Length 711;
 Best local similarity 76.5%; Pred. No. 0.0044;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLWELL 17
 Db 275 VVARSVNGKEDALWNL 291

RESULT 9
 S01384
 transferrin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C:Accession: S01384; A60520; A61573
 R:Baldwin, G.S.; Weinstock, J.
 Nucleic Acids Res. 16, 8720, 1988
 A:Title: Nucleotide sequence of porcine liver transferrin.
 A:Reference number: S01384; MUID:88335629; PMID:3419934
 A:Accession: S01384
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-696 <BAL>
 A:Cross-references: UNIPROT:P09571; UNIPARC:UPI00001130C2; EMBL:X12386; NID:g2126; PIDN:
 A:Note: 308-Arg was also found
 R:Baldwin, G.S.; Baccic, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, B
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A:Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine s
 A:Reference number: A60520; MUID:90227903; PMID:2328566
 A:Accession: A60520
 A:Molecule type: protein
 A:Residues: 1-8; 'X', 10-11, 'X', 13-15 <BA2>
 A:Cross-references: UNIPARC:UPI0000174485
 A:Experimental source: gastric mucosa
 A:Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upta
 R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A:Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
 A:Reference number: A61573; MUID:91293379; PMID:2065820
 A:Accession: A61573
 A:Molecule type: protein
 A:Residues: 1-8; 'X', 10-18, 'XE' <CHU>
 A:Cross-references: UNIPARC:UPI0000174486
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron transport; plasma
 F:1-696/Product: transferrin #status predicted <MAT>
 F:1-335/Domains: transferrin repeat homology <TRH1>

Query Match 75.6%; Score 65; DB 1; Length 696;
Best Local Similarity 76.5%; Pred. No. 0.0064;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 255 VVARSVNGKEDSIWELL 271

RESULT 10
A45543
Lactoferrin precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: A45543; S24173
R/Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
Anim. Genet. 23, 251-256, 1992
A/Title: Cloning and sequencing of the porcine lactoferrin cDNA.
A/Reference number: A45543; MUID:92367939; PMID:1503259
A/Accession: A45543
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-703 <ALE>
A/Cross-references: UNIPROT:P14632; UNIPARC:UPI0000177C55
A/Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBI:P111153)
R/lydon, J.P.; O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Connely, O.M.
Biochim. Biophys. Acta 1132, 97-99, 1992
A/Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
A/Reference number: S24173; MUID:92379101; PMID:1511016
A/Accession: S24173
A/Molecule type: mRNA
A/Residues: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
A/Cross-references: UNIPARC:UPI000016C6E2; EMBL:M92089; NID:9164613; PIDN:AAA31102.1; FI
A/Experimental source: mammary gland
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-703/Product: lactoferrin #status predicted <MAT>
F:20-350/Domain: transferrin repeat homology <TRH1>
F:36-48/Region: antimicrobial
F:354-691/Domain: transferrin repeat homology <TRH2>
F:28-62,38-53,129-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,48
F:17,107,206,267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
F:135/Binding site: carbonate (Arg) #status predicted
F:409,447,540,609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
F:477/Binding site: carbonate (Arg) #status predicted
F:490/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.6%; Score 65; DB 2; Length 703;
Best Local Similarity 76.5%; Pred. No. 0.0064;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 269 VVARSVNGKENSIIWELL 285

RESULT 11
A28438
Lactoferrin precursor - mouse
N/Alternate names: lactotransferrin
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A28438; A41205
R/Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
A/Reference number: A92596; MUID:87280033; PMID:3611056
A/Accession: A28438
A/Molecule type: mRNA
A/Residues: 3-707 <PEN>
A/Cross-references: UNIPARC:UPI00001744A4; EMBL:J03298

R/Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A/Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A/Reference number: A41205; MUID:92042099; PMID:1939212
A/Accession: A41205
A/Molecule type: DNA
A/Residues: 1-15 <LIU>
A/Cross-references: UNIPARC:UPI00001744A5; GB:M74778
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-707/Product: lactotransferrin #status predicted <MAT>
F:358-695/Domain: transferrin repeat homology <TRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 55; DB 1; Length 707;
Best Local Similarity 64.7%; Pred. No. 0.33;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 273 VVARSTNDKEALWELL 289

RESULT 12
A28446
transferrin - mouse (fragments)
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1989 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: A28446; A33482; B28438
R/Chen, L.H.; Bissell, M.J.
J. Biol. Chem. 262, 17247-17250, 1987
A/Title: Transferrin mRNA level in the mouse mammary gland is regulated by pregnancy and
A/Reference number: A28446; MUID:88086992; PMID:3693348
A/Accession: A28446
A/Molecule type: mRNA
A/Residues: 15-80,81-141,217-251,252-301 <CHE>
A/Cross-references: UNIPROT:O92111; UNIPARC:UPI00000E773F; UNIPARC:UPI000016D098; UNIPARC
A/Note: the authors translated the codon ACC for residue 61 as Tyr. TCC for residue 62 as
R/Izzerda, R.L.; Behringer, R.R.; Thiesen, M.; Huggenikh, J.I.; McKnight, G.S.; Brinster,
Mol. Cell. Biol. 9, 5154-5162, 1989
A/Title: Expression from the transferrin gene promoter in transgenic mice.
A/Reference number: A33482; MUID:90097932; PMID:2601714
A/Accession: A33482
A/Molecule type: DNA
A/Residues: 114,302-311 <IDZ>
A/Cross-references: UNIPARC:UPI0000177C57; UNIPARC:UPI0000177C58; GB:M30819; GB:M30820
R/Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
A/Reference number: A92596; MUID:87280033; PMID:3611056
A/Accession: B28438
A/Molecule type: mRNA
A/Residues: 86-216 <PEN>
A/Cross-references: UNIPARC:UPI000016CEB1; GB:J03299; GB:J02737; NID:9198847; PIDN:AAA394
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication

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Best Local Similarity 90.0%; Pred. No. 0.44;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 GKEDLIWELL 17
Db 81 GKEDLIWELL 90

RESULT 13
A75097
hypothetical protein PAB1598 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A75097

R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75097
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-459 <KAW>
A;Cross-references: UNIPROT:Q9UZH9, UNIPARC:UPI00000633CD, GB:AJ248286, GB:AL096836, NID
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAR1598
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH19

Query Match 57.6%; Score 49.5; DB 2; Length 459;
Best Local Similarity 52.4%; Pred. No. 1.8;
Matches 11; Conservative 3; Mismatches 2; Indels 5; Gaps 1;
QY 1 VVARSMGKEDL-----IWEI 16
Db 428 IVARDVGKEDLEDNSHWDL 448

RESULT 14
G72464
hypothetical protein APE2362 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C;Accession: G72464
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:59310339; PMID:10382966
A;Accession: G72464
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-510 <KAW>
A;Cross-references: UNIPROT:Q9Y9C5, UNIPARC:UPI000005E2FB, DDBJ:AP000064; NID:G5105945;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2362
C;Superfamily: uncharacterized conserved protein

Query Match 55.2%; Score 47.5; DB 2; Length 510;
Best Local Similarity 55.6%; Pred. No. 4.5;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
QY 1 VVARSMGK-EDLIWEI 17
Db 329 VAGPGMGEGEDLIWEVL 346

RESULT 15
S64921
probable membrane protein YLR087c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L2506
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: S64921, S64919
R;Benes, V.; Rechmann, S.; Neutwich, U.; Schwager, C.; Amorge, W.; Voss, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64921
A;Accession: S64921
A;Molecule type: DNA
A;Residues: 1-2958 <BEN>
A;Cross-references: UNIPROT:Q12150, UNIPARC:UPI000006B30B, EMBL:Z73259, NID:G1360456; PI
A;Experimental source: strain S288C
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64919
A;Accession: S64919
A;Molecule type: DNA

A;Residues: 2353-2958 <BOH>
A;Cross-references: UNIPARC:UPI000017904C, EMBL:Z73259, MIPS:YLR087C
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:CSF1
A;Cross-references: SGD:S0004077
A;Map position: 12R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YLR087c
C;Keywords: transmembrane protein
F;21-37/Domain: transmembrane #status predicted <TW1>
F;1219-1235/Domain: transmembrane #status predicted <TW2>
F;1928-1944/Domain: transmembrane #status predicted <TW3>
F;2654-2670/Domain: transmembrane #status predicted <TW4>

Query Match 52.3%; Score 45; DB 2; Length 2958;
Best Local Similarity 41.2%; Pred. No. 83;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 VVARSMGKEDLIWEI 17
Db 1653 LMSRTVGSRVSLIWEI 1669

Search completed: June 13, 2006, 04:20:34
Job time : 18.25 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:58:38 ; Search time 137.25 Seconds
(without alignments)
114.574 Million cell updates/sec

Title: US-10-612-162A-1
Perfect score: 86
Sequence: 1 VVARSWGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_7.2:*
1: UniProt_sprot:*
2: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	81	2	Q9GL90 BALMY
2	86	100.0	81	2	Q9GL95 PHOPH
3	86	100.0	697	2	Q5R9L7 PONPY
4	86	100.0	698	1	TRFE_HUMAN
5	86	100.0	698	2	Q53H26 HUMAN
6	82	95.3	81	2	Q9GL91 ZIPCA
7	82	95.3	81	2	Q9GL92 MESPE
8	82	95.3	153	2	Q3YAS1 MACMU
9	80	93.0	698	2	Q4R5M1 MACFA
10	80	93.0	81	2	Q9GL94 INIGE
11	79	91.9	81	2	Q9GL93 PHYCA
12	76	88.4	704	1	TRFE_BOVIN
13	76	87.2	695	1	TRFE_RABIT
14	75	83.7	704	1	ICA_PIG
15	72	83.7	694	2	Q7TSX8 MARMO
16	72	83.7	708	1	TRFL_CAMDR
17	71	82.6	117	2	Q6LC78 BOVIN
18	71	82.6	681	2	Q6LBN7 BOVIN
19	71	82.6	708	1	TRFL_BOVIN
20	71	82.6	708	1	TRFL_BUBBU
21	71	82.6	708	1	Q6LECT BOVIN
22	71	82.6	711	2	Q9XT72 TRIUV
23	70	81.4	708	1	TRFL_CAPII
24	70	81.4	708	2	Q5MJE8 SHEEP
25	68	79.1	189	2	Q9TQV8 HORSE
26	68	79.1	706	1	TRFE_HORSE
27	67	77.9	79	2	Q9GL89 HIPAM
28	67	77.9	695	1	TRFL_HORSE
29	67	77.9	697	1	TRFE_MOUSE
30	67	77.9	697	2	Q3UBW7 MOUSE
31	67	77.9	697	2	Q58BE9 MOUSE

32	66	76.7	698	1	TRFE_RAT	P12346 rattus norv
33	66	76.7	698	2	Q7TN70_RAT	Q7TN70 rattus norv
34	66	76.7	709	2	Q2TUW9_HUMAN	Q2TUW9 homo sapien
35	66	76.7	710	1	TRFL_HUMAN	P02788 homo sapien
36	66	76.7	711	2	Q5DSM0_HUMAN	Q5DSM0 homo sapien
37	66	76.7	711	2	Q5DKS1_HUMAN	Q5DKS1 homo sapien
38	66	76.7	979	2	Q7TMC7_RAT	Q7TMC7 rattus norv
39	66	76.7	980	2	Q7TP24_RAT	Q7TP24 rattus norv
40	65	75.6	696	1	TRFE_PIG	P09571 sus scrofa
41	65	75.6	704	1	TRFL_PIG	P14632 sus scrofa
42	65	75.6	704	2	Q6Y139_PIG	Q6Y139 sus scrofa
43	65	75.6	704	2	Q8MMN8_PIG	Q8MMN8 sus scrofa
44	60	69.8	704	2	Q7YS20_PIG	Q7YS20 sus scrofa
45	56	65.1	462	2	Q6Q147_RAT	Q6Q147 rattus norv

ALIGNMENTS

RESULT 1
ID Q9GL90 BALMY PRELIMINARY; PRT; 81 AA.
AC Q9GL90:
DT 01-MAR-2001, integrated into UniProtKB/Trembl.
DT 01-FEB-2005, sequence version 2.
DT 07-FEB-2006, entry version 20.
DE Transferrin (Fragment).
OS Balaena mysticetus (Bowhead whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Mysticeti; Balaenidae; Balaena.
OX NCBI_TaxID=27602;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481910; PubMed=1102733; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Minkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).

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CC EMBL: AF304105; AAC32047.1; -; Genomic DNA.
DR SRR: Q9GL90; 1-80.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; F:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001156; Peptidase S60.
DR PANTHER: PTHR11485; Peptidase S60; 1.
DR Pfam: PF00405; Transferrin_1.
DR PRINTS: PR00422; TRANSFERRIN.
DR PROSITE: PS00207; TRANSFERRIN_3; 1.
FT NON TER 1 1
FT NON TER 81 81
SQ SEQUENCE 81 AA; 9226 MW; 3C7FEDB3AF2FA6 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 39 VVARSWGKEDLIWELL 55

RESULT 2
ID Q9GL95 PHOPH PRELIMINARY; PRT; 81 AA.
AC Q9GL95:

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DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Transferrin (Fragment).
OS Phocoenocetes phocoena (Harbor porpoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=9742;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Cassens I., Vicario S., Maddell V.G., Balciowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Baetida R., Meyer A.,
RA Stanhope M.J., Milinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
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CC -----
CC EMBL: AF304100; AAG32042.1; -; Genomic_DNA.
CC
DR HSSP: P09571; 1H76.
DR SMR: O9GL95; 1-81.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001156; Peptidase S60.
DR PANTHER: PTHR11485; Peptidase S60; 1.
DR Pfam: PF00405; Transferrin_1.
DR PRINTS: PR00422; TRANSFERRIN.
DR 4
FT NON_TER 1
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FT SEQUENCE 81 AA; 9379 MW; 7B5DE6D52445A45 CRC64;
SQ

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Query Match 100.0%; Score 86; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSMGKEDLIWELL 55

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RESULT 3
Q5R9L7_PONPY PRELIMINARY; PRT; 697 AA.
AC Q5R9L7;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein DKFZp459H0229.
GN Name=DKFZp459H0229.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German CDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Oeinger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL: CR859370; CA91543.1; -; mRNA.
DR SMR: Q5R9L7; 23-346.

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DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001156; Peptidase S60.
DR PANTHER: PTHR11485; Peptidase S60; 1.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER_2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
DR Hypothetical protein.
SQ SEQUENCE 697 AA; 77010 MW; 3567442528842833 CRC64;

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Query Match 100.0%; Score 86; DB 2; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 VVARSMGKEDLIWELL 17
DB 270 VVARSMGKEDLIWELL 286

```

RESULT 4
TRFE_HUMAN STANDARD; PRT; 698 AA.
ID TRFE_HUMAN
AC P02787; O43890; Q9NOB8; Q9UNV0;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1989, sequence version 2.
DT 07-MAR-2006, entry version 84.
DE Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal)-
DE binding globulin).
GN Name=TF; ORFNames=PRO1400;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS TF*B2; TF*CHI AND TF*DI.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
RA van Bragt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal
RT localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,
RA Chamoun P., Cohen G.N., Zakin M.W.;
RT "Complete structure of the human transferrin gene. Comparison with
RT analogous chicken gene and human pseudogene.";
RL Gene 56:109-116(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92231399; PubMed=1809186;
RA Hershenberger C.L., Larson J.L., Arnold B., Roestek P.R. Jr.,
RA Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W., Tice P.A.;
RT "A cloned gene for human transferrin.";
RL Ann. N.Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=11110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
RA Fairbanks V.F.;
RT "Molecular characterization of a case of atransferrinemia.";
RL Blood 96:4071-4074(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,

RA Ahearn M.O., Kuldaneck S.A., Rajkumar N., Toch E.J., Yi Q.,
 RA Nickerson D.A.,
 RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
 RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Raha S.S., Loquiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 99-698.
 RC TISSUE=Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.,
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 422-698.
 RX MEDLINE=84153910; PubMed=6322780;
 RA Uzan G., Fraim M., Park I., Besmond C., Maessen G., Trepatt J.S.,
 RA Zakin M.M., Kahn A.,
 RT "Molecular cloning and sequence analysis of cDNA for human
 RT transferrin.";
 RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
 RN [9]
 RP PROTEIN SEQUENCE OF 20-698.
 RX MEDLINE=83160878; PubMed=6833213;
 RA McGillivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
 RA Lineback-Zins J., Brew K.,
 RT "The primary structure of human serum transferrin. The structures of
 RT seven chymogen bromide fragments and the assembly of the complete
 RT structure.";
 RL J. Biol. Chem. 258:3543-3553(1983).
 RN [10]
 RP NUCLEOTIDE SEQUENCE OF 73-698.
 RX MEDLINE=85216459; PubMed=3858812;
 RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
 RA Zakin M.M.,
 RT "Organization of the human transferrin gene: direct evidence that it
 RT originated by gene duplication.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 1-14.
 RX MEDLINE=87066744; PubMed=3786138;
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.,
 RT "The 5' region of the human transferrin gene: structure and potential
 RT regulatory sites.";
 RL Nucleic Acids Res. 14:8692-8692(1986).
 RN [12]
 RP NUCLEOTIDE SEQUENCE OF 1-72 AND 291-300.
 RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
 RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.,

RT "The human transferrin gene: 5' region contains conserved sequences
 RT which match the control elements regulated by heavy metals,
 RT glucocorticoids and acute phase reaction.";
 RL Gene 49:167-175(1986).
 RN [13]
 RP NUCLEOTIDE SEQUENCE OF 45-72.
 RX MEDLINE=20392111; PubMed=10931525;
 RX DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNRS53.0.CO;2-O;
 RA de Aribia Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
 RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.,
 RT "Alternative splicing prevents transferrin secretion during
 RT differentiation of a human oligodendrocyte cell line.";
 RL J. Neurosci. Res. 61:388-395(2000).
 RN [14]
 RP NUCLEOTIDE SEQUENCE OF 564-624, AND VARIANT TF*C2.
 RC TISSUE=Brain;
 RX MEDLINE=97418135; PubMed=9272172; DOI=10.1007/s004390050533;
 RA Namekata K., Oyama F., Imagawa M., Ihara Y.,
 RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
 RT C1 or Tf C2 variant.";
 RL Hum. Genet. 100:457-458(1997).
 RN [15]
 RP NUCLEOTIDE SEQUENCE OF 564-624.
 RA Tsuchida S., Ikemoto S., Kajii E.,
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP NUCLEOTIDE SEQUENCE OF 636-696.
 RX MEDLINE=89386721; PubMed=2780570;
 RA Duguid J.R., Belmont C.W., Liu N.G., Tourtelotte W.W.,
 RT "Changes in brain gene expression shared by scrapie and Alzheimer
 RT disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
 RN [17]
 RP PROTEIN SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalov E.S., Shishkin S.S., Efimochkin A.S., Kovalova M.A.,
 RA Ershova L.I., Egorov T.A., Musalyamov A.K.,
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [18]
 RP DISULFIDE BONDS.
 RX MEDLINE=82222166; PubMed=6953407;
 RA McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
 RA Lineback-Zins J., Brew K.,
 RT "The complete amino acid sequence of human serum transferrin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
 RN [19]
 RP MUTAGENESIS.
 RX MEDLINE=92031536; PubMed=1932003;
 RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.,
 RT "Expression and initial characterization of five site-directed mutants
 RT of the N-terminal half-molecule of human transferrin.";
 RL Biochemistry 30:10824-10829(1991).
 RN [20]
 RP CARBOHYDRATE-LINKAGE SITES ASN-432 AND ASN-630.
 RX PubMed=1335952; DOI=10.1021/PRO502065;
 RA Liu T., Qian W.-J., Griltsenko M.A., Camp D.G. II, Monroe M.E.,
 RA Moore R.J., Smith R.D.,
 RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
 RT hydrazide chemistry, and mass spectrometry.";
 RL J. Proteome Res. 4:2070-2080(2005).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
 RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/bi980355j;
 RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
 RA Woodworth R.C., Brayer G.D., Baker E.N.,
 RT "Two high-resolution crystal structures of the recombinant N-lobe of
 RT human transferrin reveal a structural change implicated in iron
 RT release.";
 RL Biochemistry 37:7919-7928(1998).

```

RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/bi9812064;
RA Jeffrey P.D., Bewley M.C., Macgillivray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Ligand-induced conformational change in transferrin: crystal
RT structure of the open form of the N-terminal half-molecule of human

Query Match 100.0%; Score 86; DB 1; Length 698;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 270 VVARSMGKEDLIWELL 286

RESULT 5
Q53H26 HUMAN PRELIMINARY; PRT; 698 AA.
ID Q53H26;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Transferrin variant (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=9411032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=9803896; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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EMBL AK222755; BAD96475.1; -; mRNA.
DR SMR; Q53H26; 23-346.
DR Ensembl; ENSG00000091513; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006826; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER_2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
FT NON_TER 1
FT SEQUENCE 698 AA; 77080 MW; A54775D23B9A4FFF CRC64;
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Query Match 100.0%; Score 86; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 270 VVARSMGKEDLIWELL 286

RESULT 6
Q9GL91 ZIPCA PRELIMINARY; PRT; 81 AA.
ID Q9GL91;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE Transferrin (Fragment).
OS Ziphius cavirostris (goose-beaked whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Ziphiidae; Ziphius.
NCBI_Taxid=9760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Cassens I., Vicario S., Madrell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Baetida R., Meyer A.,
RA Stanhope M.J., Milinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347 (2000).
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EMBL AF304104; AAC32046.1; -; Genomic_DNA.
DR HSP; P02787; 1ABE.
DR SMR; Q9GL91; 1-80.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006826; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
FT NON_TER 81
FT SEQUENCE 81 AA; 9244 MW; D6BE22BB22C8E3B3 CRC64;

Query Match 95.3%; Score 82; DB 2; Length 81;
Best Local Similarity 94.1%; Pred. No. 6.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSMGKEDLIWELL 55

RESULT 7
Q9GL92 MESPE PRELIMINARY; PRT; 81 AA.
ID Q9GL92;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 14.
DE Transferrin (Fragment).
OS Mesopiodon peruvianus (Peruvian beaked whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Ziphiidae; Mesopiodon.
NCBI_Taxid=27617;
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Cessena I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Mohan L., Simoes-Lopes P.C., Baetida R., Meyer A.,
RA Stanhope M.J., Milkovitch M.C.
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
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DR EMBL; AF304103; AAC32045.1; -; Genomic_DNA.
DR HSSP; P02787; 10QF.
DR SMR; Q9GJ92; 1-81.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR01156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 81 AA; 9138 MW; 1DC9418BF5FEACC3 CRC64;

Query March 95.3%; Score 82; DB 2; Length 81;
Best Local Similarity 94.1%; Pred. No. 6.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWELL 17
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Db 39 VVARSVGKEDLIWELL 55

RESULT 8
Q3YAS1 MACMU PRELIMINARY; PRT; 153 AA.
ID Q3YAS1 MACMU
AC Q3YAS1;
DT 27-SEP-2005; Integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005; Sequence version 1.
DT 07-FEB-2006; Entry version 3.
DE Transferrin (Fragment).
GN Name=TF;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tkatchenko A.V., Walsh P.A., Tkatchenko T.V., Guslinich S.,
RA Ravitsky E.;
RT "Form deprivation modulates proliferation of retinal neuroprogenitor
RT cells in primate experimental myopia."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; DQ147929; AA280920.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR01156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PER. 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00206; TRANSFERRIN_3; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.

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FT NON_TER 1
FT NON_TER 153
SQ SEQUENCE 153 AA; 17082 MW; 291AB15653615C06 CRC64;

Query March 95.3%; Score 82; DB 2; Length 153;
Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWELL 17
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Db 91 VVARSVGKEDLIWELL 107

RESULT 9
Q4R5M1 MACFA PRELIMINARY; PRT; 698 AA.
ID Q4R5M1 MACFA
AC Q4R5M1;
DT 19-JUL-2005; Integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005; Sequence version 1.
DT 07-FEB-2006; Entry version 5.
DE Brain cDNA, clone: QCE-13766, similar to human transferrin (TF).
DE Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/mw187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5 UTR Evolution;
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs."
RL Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AB169522; BAB01604.1; -; mRNA.
DR SMR; Q4R5M1; 23-346.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR01156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PER. 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 698 AA; 77010 MW; F19A15A7C896399B CRC64;

Query March 95.3%; Score 82; DB 2; Length 698;
Best Local Similarity 94.1%; Pred. No. 6.3e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWELL 17
| | | | | | | | | | | | | | | | | | | |
Db 270 VVARSVGKEDLIWELL 286

RESULT 10
Q9GL94 INIGE PRELIMINARY; PRT; 81 AA.
ID Q9GL94 INIGE
AC Q9GL94;

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DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Transferrin (Fragment).
OS Inia geoffensis (Amazon dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Iniidae; Inia.
OX NCBI_TaxID=9725;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Cassens I., Vicario S., Waddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Baetida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
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DR EMBL: AF304101; AAC32043.1; -; Genomic_DNA.
DR HSSP: P19134; 1-81.
DR SMR: O9GL93; 1-81.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008199; F:ferri iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001156; Peptidase_S60.
DR PANTHER: PTHR11485; Peptidase_S60; 1.
DR Pfam: PF00405; Transferrin_1.
DR PRINTS: PR00422; TRANSFERRIN.
DR NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9220 MW; 49BD4339D3F1B52A CRC64;
Query Match 93.0%; Score 80; DB 2; Length 81;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSTGKEDLIWELL 55
RESULT 11
O9GL93 PHYCA PRELIMINARY; PRT; 81 AA.
AC O9GL93;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Transferrin (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Physteriidae; Physter.
OX NCBI_TaxID=9755;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Cassens I., Vicario S., Waddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Baetida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: AF304102; AAC32044.1; -; Genomic_DNA.
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DR HSSP: P19134; 1-81.
DR SMR: O9GL93; 1-81.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008199; F:ferri iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001156; Peptidase_S60.
DR PANTHER: PTHR11485; Peptidase_S60; 1.
DR Pfam: PF00405; Transferrin_1.
DR PRINTS: PR00422; TRANSFERRIN_3; 1.
DR PROSITE: PS00207; TRANSFERRIN_3; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9220 MW; 8B9DEA2153941BA6 CRC64;
Query Match 91.9%; Score 79; DB 2; Length 81;
Best Local Similarity 94.1%; Pred. No. 2.1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSMGKEDLIWELL 55
RESULT 12
TRFE BOVIN STANDARD; PRT; 704 AA.
AC Q29443;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-MAR-2006, entry version 42.
DE Sero-transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal-
DE binding globulin).
GN Name=TF;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Liver;
RX MEDLINE=96132861; PubMed=8557646; DOI=10.1074/jbc.271.2.1166;
RA Retzer M.D., Kahani A., Button L.L., Yu R.H., Schryvers A.B.;
RT "Production and characterization of chimeric transferrins for the
RT determination of the binding domains for dacterial transferrin
RT receptors."
RL J. Biol. Chem. 271:1166-1173(1996).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two Fe(3+) ions in association with the binding of an
CC anion, usually bicarbonate. It is responsible for the transport of
CC iron from sites of absorption and heme degradation to those of
CC storage and utilization. Serum transferrin may also have a further
CC role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; Protein.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- MISCELLANEOUS: The peptidase S60 domains do not have protease
CC function as the catalytic residues are missing.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
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CC -----
DR EMBL: U02564; AAA96735.1; -; mRNA.
DR HSSP: P09571; 1H76.
DR MEROPS: S60_971; -.
DR InterPro: IPR001156; Peptidase_S60.
DR PANTHER: PTHR11485; Peptidase_S60; 1.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER_2.
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DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KM Glycoprotein; Ion transport; Iron; Iron transport; Metal-binding;
KM Methylation; Repeat; Signal; Transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 704 Serotransferrin.
FT 25 351 /FTID=PRO_0000035713.
FT DOMAIN 364 689 Peptidase S60 1.
FT METAL 81 81 Iron 1 (By similarity).
FT METAL 113 113 Iron 1 (By similarity).
FT METAL 211 211 Iron 1 (By similarity).
FT METAL 272 272 Iron 1 (By similarity).
FT METAL 414 414 Iron 2 (By similarity).
FT METAL 449 449 Iron 2 (By similarity).
FT METAL 543 543 Iron 2 (By similarity).
FT METAL 611 611 Iron 2 (By similarity).
FT BINDING 138 138 Carbonate 1 (By similarity).
FT BINDING 142 142 Carbonate 1 (By similarity).
FT BINDING 144 144 Carbonate 1; via amide nitrogen (By similarity).
FT BINDING 145 145 Carbonate 1; via amide nitrogen (By similarity).
FT BINDING 475 475 Carbonate 2 (By similarity).
FT BINDING 479 479 Carbonate 2 (By similarity).
FT BINDING 481 481 Carbonate 2; via amide nitrogen (By similarity).
FT BINDING 482 482 Carbonate 2; via amide nitrogen (By similarity).
FT MOD_RES 42 42 Omega-N-methylated arginine (By similarity).
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).
FT DISULFID 28 66 By similarity.
FT DISULFID 38 57 By similarity.
FT DISULFID 136 217 By similarity.
FT DISULFID 176 192 By similarity.
FT DISULFID 179 200 By similarity.
FT DISULFID 189 202 By similarity.
FT DISULFID 250 264 By similarity.
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FT DISULFID 377 390 By similarity.
FT DISULFID 424 699 By similarity.
FT DISULFID 441 663 By similarity.
FT DISULFID 473 549 By similarity.
FT DISULFID 497 690 By similarity.
FT DISULFID 507 521 By similarity.
FT DISULFID 518 532 By similarity.
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FT DISULFID 641 646 By similarity.
SQ SEQUENCE 704 AA; 77753 MW; D87BB2AF646C708D CRC64;

Query Match 88.4%; Score 76; DB 1; Length 704;
Best Local Similarity 82.4%; Pred. No. 0.00069;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Liver.
RX MEDLINE=91274362; PubMed=2054387; DOI=10.1016/0167-4781(91)90021-D;
RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umehals T.M.,
RA Woodworth R.C., Macgillivray R.T.A.;
"\"The nucleotide sequence of rabbit liver transferrin cDNA.\"";
RT Biochim. Biophys. Acta 1089:262-265(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=New Zealand white;
RA Shareeb B.A.A., Thepot D., Puisant C., Cajero-Juarez M.,
RA Houdebine L.M.;
"\"Cloning and structural organisation of the rabbit transferrin encoding gene.\"";
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE OF 20-51.
RX MEDLINE=88209278; PubMed=3365331;
RA Godovac-Zimmermann J.;
RT "Isolation, characterization and N-terminal amino-acid sequence of rabbit transferrin.\"";
RL Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN [4]
RP PROTEIN SEQUENCE OF 483-545.
RX MEDLINE=89005676; PubMed=1169252; DOI=10.1016/0014-5793(88)80221-7;
RA Evans R.W., Aitken A., Patel K.J.;
RT "Evidence for a single glycan moiety in rabbit serum transferrin and location of the glycan within the polypeptide chain.\"";
FEBS Lett. 238:39-42(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC TISSUE=Plasma.
RX MEDLINE=89026775; PubMed=1179277;
RA Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,
RA Horsburgh C., Jhoti H., Lindley P.F., Mydin A., Satta R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.\"";
RL Biochemistry 27:5804-5812(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Satta R., Garratt R.C., Gorinsky B., Jhoti H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin: preliminary structure analysis of the N-terminal half-molecule at 2.3-A resolution.\"";
RL Acta Crystallogr. B 46:763-771(1990).
CC -I- FUNCTION: Transferrins are iron binding transport proteins which can bind two Fe(3+) ions in association with the binding of an anion, usually bicarbonate. It is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization. Serum transferrin may also have a further role in stimulating cell proliferation.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted protein.
CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -I- MISCELLANEOUS: The peptidase S60 domains do not have protease function as the catalytic residues are missing.
CC -I- SIMILARITY: Belongs to the transferrin family.
CC -I- SIMILARITY: Contains 2 peptidase S60 domains.
CC -----
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CC -----
DR EMBL; X58533; CA41424.1; -; mRNA.
DR EMBL; AF031625; AB994136.1; -; Genomic DNA.
DR EMBL; AF031611; AB994136.1; JOINED; Genomic DNA.
DR EMBL; AF031612; AB994136.1; JOINED; Genomic DNA.
DR EMBL; AF031613; AB994136.1; JOINED; Genomic DNA.
DR EMBL; AF031614; AB994136.1; JOINED; Genomic DNA.
DR EMBL; AF031615; AB994136.1; JOINED; Genomic DNA.

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DR EMBL: AF031616; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031617; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031618; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031619; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031620; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031621; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031622; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031623; AAB94136.1; JOINED; Genomic_DNA.
DR EMBL: AF031624; AAB94136.1; JOINED; Genomic_DNA.
DR PDB: 1UNF; X-ray; A=20-695.
DR PDB: 1TFD; X-ray; @=20-323.
DR MEROPS: S60.975; -.
DR linkhub; P19134; -.
DR InterPro: IPR001156; Peptidase_S60.
DR PANTHER: PTHR11485; Peptidase_S60; 1.
DR Pfam: PF00405; Transferin; 2.
DR PRINTS: PRO0422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 1.
DR PROSITE: PS00206; TRANSFERRIN_2; 1.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
DR 3D-structure; Direct protein sequencing; Glycoprotein; Ion transport;
KM Iron; Iron transport; Metal-binding; Methylation; Repeat; Signal;
Transport.
FT CHAIN 1 19
FT SIGNAL 20 695
FT DOMAIN 25 347
FT DOMAIN 361 680
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FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
FT METAL 411 411
FT METAL 444 444
FT METAL 533 533
FT METAL 601 601
FT BINDING 139 139
FT BINDING 143 143
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FT BINDING 146 146
FT BINDING 470 470
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FT BINDING 476 476
FT BINDING 477 477
FT MOD_RES 42 42
FT CARBOHYD 509 509
FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 612
FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
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FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 636
FT DISULFID 631 636
FT VARIANT 517 517
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FT STRAND 27 29

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FT HELIX 91 94
FT TURN 96 102
FT STRAND 105 105
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FT STRAND 112 112
FT STRAND 114 121
FT TURN 122 123
FT TURN 128 129
FT TURN 132 133
FT TURN 136 137
FT STRAND 139 139
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT TURN 155 157
FT STRAND 158 158
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FT TURN 240 241

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Best local Similarity 88.2%; Pred. No. 0.001;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 270 VVARSVGKEDLIWELL 286

RESULT 14
ICA_PIG STANDARD; PRT; 704 AA.
AC Q29545;
DT 15-JUL-1999, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 39.
DE Inhibitor of carbonic anhydrase precursor.
GN Name=ICA;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
NOCLCOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
RP MEDLINE=97254619; PubMed=9100029; DOI=10.1021/bj9627424;
RA Wuebbers M.W., Roush E.D., Decastro C.M., Fierke C.A.;

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RT "Cloning, sequencing, and recombinant expression of the porcine
 RT inhibitor of carbonic anhydrase: a novel member of the transferrin
 RT family.";
 RL Biochemistry 36:4327-4336(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93099129; PubMed=1463741;
 RA Roush E.D., Fierke C.A.;
 RT "Purification and characterization of a carbonic anhydrase II
 RT inhibitor from porcine plasma."
 RL Biochemistry 31:12536-12542(1992).
 CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
 CC with nanomolar affinity.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PFM: N-glycosylated.
 CC -1- MISCELLANEOUS: The peptidase S60 domains do not have protease
 CC function as the catalytic residues are missing.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -1- SIMILARITY: Contains 2 peptidase S60 domains.
 CC -----
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 CC -----
 DR EMBL, U36916; AAB58956.1; -; mRNA.
 DR F1R, 147228; 147228.
 DR HSP, P09571; 1476.
 DR LinkHub, Q29545; -;
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam, PF00405; Transferrin_2.
 DR PRINTS, PR00422; TRANSFERRIN.
 DR SMART, SM00094; TR_FER. 2.
 DR PROSITE, PS00205; TRANSFERRIN_1; 2.
 DR PROSITE, PS00206; TRANSFERRIN_2; 1.
 DR PROSITE, PS00207; TRANSFERRIN_3; 2.
 KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 704 Inhibitor of carbonic anhydrase.
 FT DOMAIN 25 347 /Frid=PRO_0000035745.
 FT DOMAIN 357 689 Peptidase_S60_1.
 FT CARBOHYD 491 491 Peptidase_S60_2.
 FT DISULFID 28 491 N-linked (GlcNAc...) (Potential).
 FT DISULFID 38 58 By similarity.
 FT DISULFID 137 213 By similarity.
 FT DISULFID 172 188 By similarity.
 FT DISULFID 175 196 By similarity.
 FT DISULFID 185 198 By similarity.
 FT DISULFID 246 260 By similarity.
 FT DISULFID 360 392 By similarity.
 FT DISULFID 370 383 By similarity.
 FT DISULFID 417 699 By similarity.
 FT DISULFID 440 662 By similarity.
 FT DISULFID 472 549 By similarity.
 FT DISULFID 496 690 By similarity.
 FT DISULFID 506 520 By similarity.
 FT DISULFID 517 532 By similarity.
 FT DISULFID 589 603 By similarity.
 SQ SEQUENCE 704 AA; 77634 MW; 16BBO651931E336 CRC64;

Query Match 87.2%; Score 75; DB 1; Length 704;
 Best Local Similarity 88.2%; Pred. No. 0.001;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 Db 270 VVARSDGKEDLIWELL 286

RESULT 15
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ID Q7TSXB_MARMO PRELIMINARY; PRT; 694 AA.
 AC Q7TSXB;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DE 07-FEB-2006, entry version 11.
 DE Transferrin.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Sciuridae; Xerinae; Marmotini; Marmota.
 OX NCBI_TaxID=9995;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Rinaudo J.A.S., Gerin J.L.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -----
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 DR EMBL, AY288100; AAP37129.1; -; mRNA.
 DR HSP, P19134; 1UNF.
 DR GO, GO:0005576; C:extracellular region; IEA.
 DR GO, GO:0008199; F:ferric iron binding; IEA.
 DR GO, GO:0006879; P:iron ion homeostasis; IEA.
 DR GO, GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Peptidase_S60.
 DR PANTHER, PTHR11485; Peptidase_S60; 1.
 DR Pfam, PF00405; Transferrin_2.
 DR PRINTS, PR00422; TRANSFERRIN.
 DR SMART, SM00094; TR_FER. 2.
 DR PROSITE, PS00205; TRANSFERRIN_1; 2.
 DR PROSITE, PS00206; TRANSFERRIN_2; 2.
 DR PROSITE, PS00207; TRANSFERRIN_3; 2.
 SQ SEQUENCE 694 AA; 76466 MW; 40053F7DC1CFCAB7 CRC64;

Query Match 83.7%; Score 72; DB 2; Length 694;
 Best Local Similarity 82.4%; Pred. No. 0.0033;
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 Db 270 VVARVDGKEDLIWELL 286

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 Job time : 137.25 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:20:54 ; Search time 30 Seconds
(without alignments)

49.601 Million cell updates/sec

Title: US-10-612-162A-1
Perfect score: 86
Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:*
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2: /EMC_Ceiera_SIDS3/prodata/2/iaa/6.COMB.pep:*
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7: /EMC_Ceiera_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	86	100.0	698	1 US-09-439-740-2	Sequence 2, Appli
4	86	100.0	1074	1 US-08-470-058-2	Sequence 2, Appli
5	86	100.0	1074	2 US-09-037-188-2	Sequence 2, Appli
6	86	100.0	1074	2 US-09-285-310-2	Sequence 2, Appli
7	86	100.0	1074	2 US-09-753-385-2	Sequence 2, Appli
8	86	100.0	1410	1 US-08-470-058-4	Sequence 4, Appli
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13	86	100.0	708	1 US-08-453-703-4	Sequence 4, Appli
14	86	100.0	708	1 US-08-456-106-4	Sequence 4, Appli
15	86	100.0	708	1 US-08-456-106-4	Sequence 4, Appli
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40	66	76.7	711	2 US-09-265-577-2	Sequence 2, Appli
41	66	76.7	711	2 US-09-633-739-2	Sequence 2, Appli
42	66	76.7	711	5 PCT-US93-03614-2	Sequence 2, Appli
43	66	75.6	703	1 US-08-145-681-6	Sequence 6, Appli
44	66	75.6	703	1 US-08-453-703-6	Sequence 6, Appli
45	66	75.6	703	1 US-08-456-106-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTLIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4:
; LENGTH: 696
5262177-4

Query Match      100.0%; Score 86; DB 7; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      270 VVARSMGKEDLIWELL 286

RESULT 2
US-08-175-158A-2
; Sequence 2, Application US/08175158A
; Patent No. 5986067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MAGGILLIWAY, Rose T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,158A
FILING DATE: 28-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,029
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-175-158A-2

Query Match      100.0%; Score 86; DB 1; Length 698;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      270 VVARSMGKEDLIWELL 286

RESULT 3
US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MAGGILLIVRAY, Ross T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODMORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
```

```
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match      100.0%; Score 86; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      270 VVARSMGKEDLIWELL 286

RESULT 4
US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TX193-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match      100.0%; Score 86; DB 1; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      646 VVARSMGKEDLIWELL 662

RESULT 5
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
```

```

;
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,188
; FILING DATE: 02-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-037-188-2

Query Match          100.0%; Score 86; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      646 VVARSMGKEDLIWELL 662

RESULT 6
US-09-285-310-2
; Sequence 2, Application US/09285310
; Patent No. 6262026
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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```

;
; APPLICATION NUMBER: US/09/285,310
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-285-310-2

Query Match          100.0%; Score 86; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      646 VVARSMGKEDLIWELL 662

RESULT 7
US-09-753-385-2
; Sequence 2, Application US/09753385
; Patent No. 6858578
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
; TITLE OF INVENTION: OF A SELECTED SUBSTANCE INTO CELLS
; FILE REFERENCE: 10278-025004
; CURRENT APPLICATION NUMBER: US/09/753,385
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 08/470,058
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 09/037,188
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 09/285,310
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1074
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-753-385-2

Query Match          100.0%; Score 86; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      646 VVARSMGKEDLIWELL 662

RESULT 8
US-08-470-058-4
; Sequence 4, Application US/08470058
; Patent No. 5817789
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
```

TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 100.0%; Score 86; DB 1; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 982 VVARSMGKEDLIWELL 998

RESULT 9
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 100.0%; Score 86; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 982 VVARSMGKEDLIWELL 998

RESULT 10
US-09-285-310-4
Sequence 4, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 100.0%; Score 86; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
Db 982 VVARSMGKEDLIWELL 998

RESULT 11
US-09-753-385-4
Sequence 4, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1410
TYPE: PRT
ORGANISM: Homo sapiens
US-09-753-385-4

Query Match 100.0%; Score 86; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3,8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
Db 982 VVARSMGKEDLIWELL 998

RESULT 12
US-08-145-681-4
Sequence 4, Application US/08145681
Patent No. 5571691
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headdon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 910 Louisiana St
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mcgregor, Martin L.

REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 19928-0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/229/1874
TELEFAX: 713/229/1522
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-145-681-4

Query Match 82.6%; Score 71; DB 1; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00072;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKL 290

RESULT 13
US-08-453-703-4
Sequence 4, Application US/08453703
Patent No. 5766939
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headdon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; US-08-453-703-4

Query Match
Best Local Similarity 82.6%; Score 71; DB 1; Length 708;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKL 290

RESULT 14
US-08-456-106-4
; Sequence 4, Application US/08456106
; Patent No. 5849881
; GENERAL INFORMATION:
; APPLICANT: Connely, Orla M.
; APPLICANT: Heaton, Denis R.
; APPLICANT: O'Malley, Bert W.
; APPLICANT: May, Gregory S.
; TITLE OF INVENTION: Production of Recombinant Lactoferrin
; TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
; TITLE OF INVENTION: Various Organisms
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,106
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/145,681
; FILING DATE: October 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8206-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; US-08-456-106-4

Query Match
Best Local Similarity 82.6%; Score 71; DB 1; Length 708;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKL 290

```

```

RESULT 15
US-08-456-108-4
; Sequence 4, Application US/08456108
; Patent No. 6100054
; GENERAL INFORMATION:
; APPLICANT: Connely, Orla M.
; APPLICANT: Heaton, Denis R.
; APPLICANT: O'Malley, Bert W.
; APPLICANT: May, Gregory S.
; TITLE OF INVENTION: Production of Recombinant Lactoferrin
; TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
; TITLE OF INVENTION: Various Organisms
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,108
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/145,681
; FILING DATE: October 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8206-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; US-08-456-108-4

Query Match
Best Local Similarity 82.6%; Score 71; DB 2; Length 708;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKL 290

Search completed: June 13, 2006, 04:25:49
Job time : 30 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:24 ; Search time 97.75 Seconds

(without alignments)
80.559 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	86	100.0	220	4	US-10-384-060-76
3	86	100.0	679	4	US-10-378-094-3
4	86	100.0	679	4	US-10-384-060-3
5	86	100.0	679	4	US-10-231-494-3
6	86	100.0	679	5	US-10-429-482-4
7	86	100.0	679	5	US-10-429-487-4
8	86	100.0	679	5	US-10-429-515-4
9	86	100.0	679	5	US-10-429-598-4
10	86	100.0	679	5	US-10-429-635-4
11	86	100.0	679	5	US-10-429-653-4
12	86	100.0	679	5	US-10-429-659-4
13	86	100.0	679	5	US-10-429-661-4
14	86	100.0	679	5	US-10-429-660-4
15	86	100.0	679	5	US-10-429-662-4
16	86	100.0	679	5	US-10-429-655-4
17	86	100.0	679	5	US-10-429-654-4
18	86	100.0	698	3	US-09-935-642-6
19	86	100.0	698	4	US-10-378-094-2
20	86	100.0	698	4	US-10-384-060-2
21	86	100.0	698	4	US-10-231-494-2
22	86	100.0	698	4	US-10-383-201-10
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24	86	100.0	698	5	US-10-887-711-2
25	86	100.0	698	5	US-10-513-523-3
26	86	100.0	698	6	US-11-177-506-46
27	86	100.0	698	6	US-11-038-901-2

28	86	100.0	1074	3	US-09-753-385-2	Sequence 2, Appli
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31	86	100.0	1418	5	US-10-473-127-804	Sequence 4, Appli
32	76	88.4	704	4	US-10-513-523-4	Sequence 8, Appli
33	71	82.6	708	4	US-10-169-297-8	Sequence 4, Appli
34	71	82.6	708	5	US-10-620-256-4	Sequence 2, Appli
35	71	82.6	708	5	US-10-513-523-2	Sequence 183, App
36	69	80.2	22	5	US-10-801-990-183	Sequence 5324, App
37	66	76.7	100	3	US-09-864-408A-5324	Sequence 241, App
38	66	76.7	100	3	US-10-408-765A-241	Sequence 49, Appli
39	66	76.7	359	4	US-10-169-297-49	Sequence 4, Appli
40	66	76.7	690	4	US-10-076-816-4	Sequence 4, Appli
41	66	76.7	690	4	US-10-077-381-4	Sequence 4, Appli
42	66	76.7	690	4	US-10-639-835-4	Sequence 2, Appli
43	66	76.7	694	4	US-10-023-096-2	Sequence 273, App
44	66	76.7	695	4	US-10-316-253-773	Sequence 275, App
45	66	76.7	698	4	US-10-316-253-275	

ALIGNMENTS

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RESULT 1
; Sequence 1, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDFT)-specific
; TITLE OF INVENTION: antibodies, their preparation and use
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 02011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-612-162-1

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Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
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Db       1 VVARSMGKEDLIWELL 17

RESULT 2
US-10-384-060-76
; Sequence 76, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADBGT, Homayoun
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
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; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mtf sequence in PREX0080
; US-10-384-060-76

Query Match 100.0%; Score 86; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 183 VVARSMGKEDLIWELL 199

RESULT 3
; US-10-378-094-3
; Sequence 3, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
; US-10-378-094-3

Query Match 100.0%; Score 86; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 4
; US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494

; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
; US-10-384-060-3

Query Match 100.0%; Score 86; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 5
; US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
; US-10-231-494-3

Query Match 100.0%; Score 86; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 6
; US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tumor
; FILE REFERENCE: 2537,000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-482-4

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Query Match	100.0%;	Score 86;	DB 5;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 1.1e-05;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 VVARSMGGKEDLIWELL 17
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Db      251 VVARSMGGKEDLIWELL 267
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RESULT 7
US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment of Tumors
; FILE REFERENCE: 2531.000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-429-497-4

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Query Match	100.0%;	Score 86;	DB 5;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 1.1e-05;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db     251 VVARSMGKEDLIWELL 267
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RESULT 8
US-10-429-515-4
: Sequence 4, Application US/10429515
: Publication No. US20040219099A1
: GENERAL INFORMATION:
: APPLICANT: Sandhu, Jasbir
: TITLE OF INVENTION: Methods For The Treatment Of Tumors
: FILE REFERENCE: 2537.000005
: CURRENT APPLICATION NUMBER: US/10/429,515
: CURRENT FILING DATE: 2003-05-02
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 679
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-429-515-4

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Query Match      100.0%; Score 86; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
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Db      251 VVARSMGKEDLIWELL 267
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RESULT 9
US-10-429-598-4
; Sequence 4, Application US/104295598
; Publication No. US20040219100A1
; GENERAL INFORMATION:

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: APPLICANT: Sandhu, Jasbir
: TITLE OF INVENTION: Composition Useful For The Treatment of Tumors
: FILE REFERENCE: 2537.000003
: CURRENT APPLICATION NUMBER: US/10/429,598
: CURRENT FILING DATE: 2003-05-02
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 679
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-429-598-4

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Query Match	100.0%	Score 86;	DB 5;	Length 679;
Best Local Similarity	100.0%	Pred. No. 1.1e-05;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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OY      1 VVARSMGKEDLIWELL 17
         |||||
Db      251 VVARSMGKEDLIWELL 267

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RESULT 10
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537, 000007
; CURRENT APPLICATION NUMBER: US/10/429, 635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4

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Query Match	100.0%	Score 86;	DB 5;	Length 679;
Best Local Similarity	100.0%	Pred. No. 1.1e-05;		
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0Y      1 VVARSMGKEDLIWELL 17
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Db      251 VVARSMGKEDLIWELL 267

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RESULT 11
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jaabir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-429-653-4

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Query Match	100.0%	Score 86;	DB 5;	Length 679;
Best Local Similarity	100.0%	Pred. No. 1.1e-05;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 VVARSMMGGKEDLIWELL 17
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Db 251 VVARSMGKEDLIWELL 267

RESULT 12
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537,000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4

Query Match 100.0%; Score 86; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
Db 251 VVARSMGKEDLIWELL 267

RESULT 13
US-10-429-661-4
; Sequence 4, Application US/10429661
; Publication No. US20040219104A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Treatment Of Tumors
; FILE REFERENCE: 2537,000008
; CURRENT APPLICATION NUMBER: US/10/429,661
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-661-4

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Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
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Db 251 VVARSMGKEDLIWELL 267

RESULT 14
US-10-429-660-4
; Sequence 4, Application US/10429660
; Publication No. US20040220084A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Nucleic Acid Delivery
; FILE REFERENCE: 2537,000012
; CURRENT APPLICATION NUMBER: US/10/429,660
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-429-660-4

Query Match 100.0%; Score 86; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
Db 251 VVARSMGKEDLIWELL 267

RESULT 15
US-10-429-662-4
; Sequence 4, Application US/10429662
; Publication No. US20040220085A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Nucleic Acid Delivery
; FILE REFERENCE: 2537,000010
; CURRENT APPLICATION NUMBER: US/10/429,662
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-662-4

Query Match 100.0%; Score 86; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
Db 251 VVARSMGKEDLIWELL 267

Search completed: June 13, 2006, 04:56:24
Job time : 98.75 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:58 ; Search time 5.75 Seconds
(without alignments)
37.380 Million cell updates/sec

Title: US-10-612-162A-1
Perfect score: 86
Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BL0SUM62
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Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pap:*
4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pap:*
5: /EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pap:*
6: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pap:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	371	6 US-10-515-429-63	Sequence 63, Appl
2	86	100.0	679	6 US-10-515-429-3	Sequence 3, Appl
3	86	100.0	698	6 US-10-515-429-2	Sequence 2, Appl
4	76	88.4	685	6 US-10-515-429-41	Sequence 31, Appl
5	75	87.2	676	6 US-10-515-429-37	Sequence 37, Appl
6	72	83.7	708	7 US-11-258-767-23	Sequence 23, Appl
7	72	83.7	708	7 US-11-258-767-24	Sequence 24, Appl
8	71	82.6	681	7 US-11-258-767-13	Sequence 13, Appl
9	71	82.6	708	7 US-11-258-767-16	Sequence 16, Appl
10	71	82.6	708	7 US-11-258-767-19	Sequence 19, Appl
11	71	82.6	708	7 US-11-258-767-22	Sequence 22, Appl
12	71	82.6	708	7 US-11-258-767-29	Sequence 29, Appl
13	71	82.6	708	7 US-11-258-767-35	Sequence 35, Appl
14	71	82.6	708	7 US-11-258-767-38	Sequence 38, Appl
15	71	82.6	708	7 US-11-258-767-39	Sequence 39, Appl
16	70	81.4	708	7 US-11-258-767-28	Sequence 28, Appl
17	70	81.4	708	7 US-11-258-767-32	Sequence 32, Appl
18	68	79.1	688	6 US-10-515-429-40	Sequence 40, Appl
19	67	77.9	677	6 US-10-515-429-39	Sequence 39, Appl
20	67	77.9	695	6 US-11-258-767-26	Sequence 26, Appl
21	66	76.7	698	6 US-10-515-429-38	Sequence 38, Appl
22	66	76.7	698	6 US-11-258-767-25	Sequence 25, Appl
23	66	76.7	709	7 US-11-258-767-31	Sequence 31, Appl
24	66	76.7	710	7 US-11-258-767-33	Sequence 33, Appl
25	66	76.7	711	7 US-11-258-767-12	Sequence 12, Appl

26	66	76.7	711	7 US-11-258-767-15	Sequence 15, Appl
27	66	76.7	711	7 US-11-258-767-17	Sequence 17, Appl
28	66	76.7	711	7 US-11-258-767-18	Sequence 18, Appl
29	66	76.7	711	7 US-11-258-767-21	Sequence 21, Appl
30	66	76.7	711	7 US-11-258-767-27	Sequence 27, Appl
31	66	76.7	711	7 US-11-258-767-30	Sequence 30, Appl
32	66	76.7	711	7 US-11-258-767-34	Sequence 34, Appl
33	65	75.6	696	6 US-10-515-429-42	Sequence 42, Appl
34	65	75.6	703	7 US-11-258-767-37	Sequence 37, Appl
35	60	69.8	686	7 US-11-258-767-36	Sequence 36, Appl
36	55	64.0	707	7 US-11-258-767-14	Sequence 14, Appl
37	55	64.0	707	7 US-11-258-767-20	Sequence 20, Appl
38	41	47.7	581	7 US-11-189-279-18	Sequence 18, Appl
39	41	47.7	601	7 US-11-189-279-17	Sequence 17, Appl
40	41	47.7	634	7 US-11-189-279-16	Sequence 16, Appl
41	41	47.7	654	7 US-11-189-279-15	Sequence 15, Appl
42	40	46.5	176	6 US-10-953-349-34873	Sequence 34873, A
43	40	46.5	177	6 US-10-953-349-34872	Sequence 34872, A
44	40	46.5	206	6 US-10-953-349-34871	Sequence 34871, A
45	38	44.2	146	7 US-11-055-093-225	Sequence 225, App

ALIGNMENTS

RESULT 1
US-10-515-429-63
Sequence 63, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-MO
CURRENT APPLICATION NUMBER: US/10/515, 429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 371
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: N-domain of transferrin modified for cloning into M13-pUC18
US-10-515-429-63
Query Match 100.0%; Score 86; DB 6; Length 371;
Best Local Similarity 100.0%; Pred. No. 3, 7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSMGKEDLIWELL 290
RESULT 2
US-10-515-429-3
Sequence 3, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun

```

; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; APPLICANT: Sadeghi, Homayoun
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
US-10-515-429-3
```

```

Query Match          100.0%; Score 86; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 7,2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

1 VVARSMGKEDLIWELL 17
|||||
Db          251 VVARSMGKEDLIWELL 267
```

```

RESULT 3
US-10-515-429-2
; Sequence 2, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-515-429-2
```

```

Query Match          100.0%; Score 86; DB 6; Length 698;
Best Local Similarity 100.0%; Pred. No. 7,5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY          1 VVARSMGKEDLIWELL 17
|||||
Db          270 VVARSMGKEDLIWELL 286
```

```

RESULT 4
US-10-515-429-41
; Sequence 41, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 41
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-515-429-41
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Query Match          88.4%; Score 76; DB 6; Length 685;
Best Local Similarity 82.4%; Pred. No. 3,4e-05;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```

QY          1 VVARSMGKEDLIWELL 17
|||||
Db          255 VVARIVGKEDVIWELL 271
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```

RESULT 5
US-10-515-429-37
; Sequence 37, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-515-429-37
```

```

Query Match          87.2%; Score 75; DB 6; Length 676;
Best Local Similarity 88.2%; Pred. No. 4,9e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```

QY          1 VVARSMGKEDLIWELL 17
|||||
Db          251 VVARSVGKEDLIWELL 267
```

```

RESULT 6
US-11-258-767-23
; Sequence 23, Application US/11258767
; Publication No. US20060094082A1
```

;; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 708
; TYPE: PRT
; ORGANISM: CAMEL
US-11-258-767-23

Query Match 83.7%; Score 72; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00016;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKLL 290

RESULT 7
US-11-258-767-24

; Sequence 24, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 708
; TYPE: PRT
; ORGANISM: CAMEL
US-11-258-767-24

Query Match 83.7%; Score 72; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00016;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKLL 290

RESULT 8
US-11-258-767-13
; Sequence 13, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26

;; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 681
; TYPE: PRT
; ORGANISM: COW
US-11-258-767-13

Query Match 82.6%; Score 71; DB 7; Length 681;
Best Local Similarity 82.4%; Pred. No. 0.00023;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 247 VVARSVGKEDLIWKLL 263

RESULT 9
US-11-258-767-16

; Sequence 16, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COW
US-11-258-767-16

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSVGKEDLIWKLL 290

RESULT 10
US-11-258-767-19

; Sequence 19, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 708
; TYPE: PRT
; ORGANISM: WATER BUFFALO
US-11-258-767-19

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSDGKEDLIWKLL 290

RESULT 11

US-11-258-767-22
; Sequence 22, Application US/11258767
; Publication No. US2006094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COM
US-11-258-767-22

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSDGKEDLIWKLL 290

RESULT 12

US-11-258-767-29
; Sequence 29, Application US/11258767
; Publication No. US2006094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COM
US-11-258-767-29

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSDGKEDLIWKLL 290

RESULT 13
US-11-258-767-35
; Sequence 35, Application US/11258767
; Publication No. US2006094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COM
US-11-258-767-35

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSDGKEDLIWKLL 290

RESULT 14

US-11-258-767-38
; Sequence 38, Application US/11258767
; Publication No. US2006094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COM
US-11-258-767-38

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 274 VVARSDGKEDLIWKLL 290

RESULT 15

US-11-258-767-39
; Sequence 39, Application US/11258767
; Publication No. US2006094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel

; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COM
; US-11-258-767-39

Query Match 82.6%; Score 71; DB 7; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.00024;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VVARSMGKEDLIWELL 17
|||: |||||:
Db 274 VVARSVDGKEDLIWKLL 230

Search completed: June 13, 2006, 04:56:53
Job time : 5.75 secs

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CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 86; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
 |||||
 1 VVARSMGKEDLIWELL 17

RESULT 2

ADRI5903
 ID ADRI5903 standard; peptide; 17 AA.

XX ADR15903;

XX 04-NOV-2004 (first entry)

XX Transferrin peptide fragment #61.

XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX Synthetic.

XX WO2004070389-A1.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004MO-GB000480.

XX 06-FEB-2003; 2003GB-00002740.

XX (AXIS-) AXIS-SHIELD ASA.

XX Rye PD;

XX WPI; 2004-625547/60.

PT Assay for differentiating protein isoforms to determine their
 PT concentrations in sample e.g. blood, involves contacting the sample with
 PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
 PT detecting.

XX Disclosure; Page 15; 30pp; English.

CC The present invention describes an assay for a protein having at least
 CC two isoforms with different glycosylation patterns. The assay involves
 CC contacting a sample containing the protein with a proteolytic enzyme,
 CC followed by detecting the content or relative content of at least one
 CC peptide fragment produced by proteolysis. Also described is a kit for the
 CC assay method comprising the proteolytic enzyme and a substrate bound
 CC specific binding partner (S1) for at least 2 of the isoforms of the
 CC proteins. The method can be used for assaying isoforms of proteins
 CC according to their glycosylation pattern to determine their concentration
 CC or relative concentration in the sample or material (e.g. blood). The
 CC method avoids use of antibodies for distinguishing between glycosylated
 CC isoforms of the proteins. The present sequence represents a transferrin
 CC peptide fragment which is used in the exemplification of the present
 CC invention.

XX Sequence 17 AA;

Query Match 50.0%; Score 43; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EDLIWELL 17
 |||||
 1 EDLIWELL 8

RESULT 3

ADRI5963
 ID ADRI5963 standard; peptide; 17 AA.

XX ADR15963;

XX 04-NOV-2004 (first entry)

XX Transferrin peptide fragment #121.

XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX Synthetic.

XX WO2004070389-A1.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004MO-GB000480.

XX 06-FEB-2003; 2003GB-00002740.

XX (AXIS-) AXIS-SHIELD ASA.

XX Rye PD;

XX WPI; 2004-625547/60.

PT Assay for differentiating protein isoforms to determine their
 PT concentrations in sample e.g. blood, involves contacting the sample with
 PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
 PT detecting.

XX Disclosure; Page 17; 30pp; English.

CC The present invention describes an assay for a protein having at least
 CC two isoforms with different glycosylation patterns. The assay involves
 CC contacting a sample containing the protein with a proteolytic enzyme,
 CC followed by detecting the content or relative content of at least one
 CC peptide fragment produced by proteolysis. Also described is a kit for the
 CC assay method comprising the proteolytic enzyme and a substrate bound
 CC specific binding partner (S1) for at least 2 of the isoforms of the
 CC proteins. The method can be used for assaying isoforms of proteins
 CC according to their glycosylation pattern to determine their concentration
 CC or relative concentration in the sample or material (e.g. blood). The
 CC method avoids use of antibodies for distinguishing between glycosylated
 CC isoforms of the proteins. The present sequence represents a transferrin
 CC peptide fragment which is used in the exemplification of the present
 CC invention.

XX Sequence 17 AA;

Query Match 50.0%; Score 43; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EDLIWELL 17
 |||||
 1 EDLIWELL 8

RESULT 4

ADSI3216
 ID ADSI3216 standard; peptide; 17 AA.

XX ADSI3216;

XX	25-JUL-2003; 2003US-0490149P.
FR	
XX	(BEYO-) BEYOND GENOMICS INC.
PA	
XX	Regnier FE, Ademec J, Zhang X;
PI	
XX	WPI; 2005-162781/17.
DR	
XX	Analyzing mixture of proteins by sequencing portions of peptides in two
PT	or more sets of peptides from several peptides, to produce data set,
PT	determining likelihood of presence of proteins in mixture of proteins
PI	based on data sets.
PS	
XX	Example 4; SEQ ID NO 238; 140bp; English.
CC	
CC	The invention relates to a novel method for analyzing a mixture of
CC	proteins. The method involves selecting sets of peptides from several
CC	peptides, sequencing one or more portions of the peptides in two or more
CC	sets of peptides, to produce a data set, and determining the likelihood
CC	of the presence of two or more proteins in the mixture of proteins based
CC	on two or more data sets. The invention further comprises an article of
CC	manufacture comprising a computer-readable media with computer-readable
CC	instructions for carrying out the method. The method is useful for
CC	analyzing a mixture of proteins. The method is useful for screening and
CC	characterization of protein mixtures. This sequence represents a human
CC	serum albumin (HSA) peptide fragment used in the novel protein analysis
CC	method of the invention.
XX	
SO	Sequence 17 AA;
QY	
Db	
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 EDLIWELL 17
Db	1 EDLIWELL 8
QY	50.0%; Score 43; DB 9; Length 17;
Db	Best Local Similarity 100.0%; Pred. No. 5.4;
QY	Matches

XX
PS Example 65; SEQ ID NO 85; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel protein (161P2F10B) and its variants
CC having a sequence of 875 amino acids provided in the specification. The
CC protein of the invention is over-expressed in certain cancers. The
CC compounds of the invention may have cytostatic activity and the sequence
CC of the 161P2F10B protein, and the gene which encodes it, may be useful
CC for gene therapy or the development of a vaccine. The composition and
CC methods of the invention are useful in diagnosing, preventing and
CC treating cancer. The present sequence is the amino acid sequence of a
CC peptide derived from the human 161P2F10B variant 3 protein and used in
CC the exemplification of the invention.
XX
SQ Sequence 17 AA;
XX
Query Match 34.9%; Score 30; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 GSKEDLIW 14
|||:|
9 GSKPEALW 16
DB
RESULT 7
ADM96873
ID ADM96873 standard; peptide; 17 AA.
XX
AC ADM96873;
XX
DT 29-JUL-2004 (first entry)
XX
DE Tissue factor VIIa (FVIIa) peptide antagonist #289.
XX
XX Tissue Factor VIIa; FVIIa; chronic thromboembolic disease;
KM fibrin formation; vascular disorders; deep venous thrombosis;
KM arterial thrombosis; stroke; atherosclerosis; septicemia.
XX
XX Synthetic.
OS
XX US200408767-A1.
XX
XX 06-MAY-2004.
PD
XX 30-JAN-2003; 2003US-00356257.
PF
XX 06-FEB-2002; 2002US-0355420P.
PR
XX (GETH) GENENTECH INC.
XX
XX Lazarus RA, Maun HR;
XX
XX WPI; 2004-356247/33.
DR
XX
XX New peptide, useful for preventing or treating chronic thromboembolic
PT diseases or disorders associated with fibrin formation including vascular
PT disorders, such as deep venous thrombosis, arterial thrombosis, and
PT stroke.
XX
XX Example 2; SEQ ID NO 295; 102pp; English.
XX
XX The invention relates to peptide antagonists of tissue Factor VIIa
CC (FVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
CC with the peptide in the presence of tissue factor and under conditions
CC that allow binding of the compound to FVIIa to occur. The peptides are
CC useful for preventing or treating chronic thromboembolic diseases or
CC disorders associated with fibrin formation including vascular disorders,
CC such as deep venous thrombosis, arterial thrombosis, stroke,
CC atherosclerosis, or septicemia. The present sequence represents a FVIIa
CC peptide antagonist of the invention.
XX

SQ Sequence 17 AA;
XX
Query Match 33.1%; Score 28.5; DB 8; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 7 GSKEDLIW 14
|||:|
3 GSKPEALW 11
DB
RESULT 8
AAV41871
ID AAV41871 standard; peptide; 17 AA.
XX
XX AAV41871;
XX
XX 09-DEC-1999 (first entry)
DT
XX
DE Rheumatoid arthritis diagnostic protein isoform peptide #22.
XX
XX Human; rheumatoid arthritis; RA; diagnosis; RPI, RADP, detection;
KM rheumatoid arthritis diagnostic feature; ERPI, synovial fluid;
KM rheumatoid arthritis diagnostic protein isoform; screening;
KM expression reference protein isoform; prognosis.
XX
XX Homo sapiens.
OS
XX WO947925-A2.
XX
XX 23-SEP-1999.
PD
XX 15-MAR-1999; 99WO-GB000763.
PF
XX 13-MAR-1998; 98GB-00005477.
PR
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
PI Parekh RP, Patel TP, Townsend RR;
XX
XX WPI; 1999-571871/48.
DR
XX
XX Diagnosis of human rheumatoid arthritis by two-dimensional
PT electrophoresis.
PT
XX
XX Disclosure; Page 18; 157pp; English.
PS
XX
XX A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
CC dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analysing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs) and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADP) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADPs can be used in gene therapy
CC protocols. AAV41844 to AAV42100 represent RPI peptides, AAV42101 to
CC AAV42103 represent expression reference protein isoform peptides and
CC AAV25066 to AAV25068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention
XX
SQ Sequence 17 AA;

Query Match 32.6%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 IWEEL 17
 |||||
Db 4 IWEEL 8

RESULT 9
AAE23845
ID AAE23845 standard; peptide; 17 AA.
XX
AC AAE23845;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human zsig33-gamma peptide #1.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 7..16
 /note= "Hydrophilic region"
XX
XX US200205156-A1.
XX
PD 09-MAY-2002.
XX
XX 10-MAY-2001; 2001US-00853253.
XX
XX 11-MAY-2000; 2000US-0203300P.
XX
PA (JASPER) JASPER S R.
PA (SHEP) SHEPPARD P O.
PA (DEIS) DEISHER T A.
PA (BISH) BISHOP P D.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
XX WPI; 2002-443750/47.
DR N-PSDB; AAD38243.
XX
XX ZSIG33-like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones.
XX
PS Claim 5; Page 30; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones. The
CC sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acids in samples, and therefore which patients may be in
CC need of restorative therapy. The ZSIG33 peptides are used as antigens in
CC the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-gamma peptide

XX
SQ Sequence 17 AA;
Query Match 32.6%; Score 28; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EDLIME 15
 :|:|:|
Db 3 QDIME 8

RESULT 10
AAE15890
ID AAE15890 standard; peptide; 17 AA.
XX
AC AAE15890;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human zsig33-gamma peptide #1.
XX
KW Human; zsig33-like peptide; ZSIG3P; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adreption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-gamma peptide.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 7..16
 /note= "Hydrophilic region"
XX
XX WC200187933-A2.
XX
PD 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US015091.
XX
XX 11-MAY-2000; 2000US-00569271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
XX WPI; 2002-082982/11.
DR N-PSDB; AAD25764.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and treating
PT gastrointestinal and growth related diseases, comprises zsig33-like
PT peptides.
XX
PS Claim 5a; Page 85; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZSIG3P) including zsig33-
CC linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-epsilon
CC peptides and nucleic acid molecules encoding such zsig33-like peptides.
CC ZSIG3P peptides activate the immune system in boosting immunity to
CC infectious diseases, treating immunocompromised patients such as human
CC immunodeficiency virus (HIV) patients, in improving vaccines and in
CC treatment of bacterial, viral, protozoal and fungal infections. Peptides
CC of the invention are used to identify and isolate receptors involved in
CC growth regulation in the liver, blood vessel formation and other
CC developmental processes. They are useful for evaluating functions of
CC hypothalamic-pituitary-adrenal axis, to modulate growth and/or
CC differentiation of tumour cells, as additives to anti-hypoglycaemic
CC preparations containing glucose and as adreption enhancers for oral
CC drugs which require fast nutrient action and to stimulate glucose-induced
CC insulin release. They are also useful as research reagents for the
CC expansion, differentiation, growth factor and hormone secretion and/or
CC cell-cell interactions of tissues associated with gastrointestinal

CC system, brain and central nervous system. These molecules are useful for
CC treating dysfunction associated with contractile tissues or to suppress
CC or enhance contractility in vivo and to treat gastrointestinal and growth
CC related diseases. ZS33LP peptides, nucleic acids and/or antibodies are
CC useful for treating disorders associated with gastrointestinal
CC contractility, secretion of digestive enzymes, hormone and acids,
CC secretion of hormones in the pancreas and/or brain, gastrointestinal
CC motility, recruitment of digestive enzymes, inflammation and regulation
CC of nutrient absorption. Sequences of the invention are useful in gene
CC therapy. The present sequence is human zsi933-gamma peptide
CC
SQ Sequence 17 AA;

Query Match 32.6%; Score 28; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EDLWME 15
:|::|
Db 3 QDILWE 8

RESULT 11
ABG72317
ID ABG72317 standard; peptide; 17 AA.
XX
AC ABG72317;
XX
XX 29-JAN-2003 (first entry)
XX
DE Human pro-apoptotic protein DIABLO peptide sequence #13.
XX
XX Human; pro-apoptotic protein; DIABLO; cell death; apoptosis;
XX inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic disease;
XX autoimmune disease; neurodegenerative disease; tissue damage;
XX muscular tissue damage; heart attack; hepatic tissue damage;
XX liver disease; immunogen.
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note="Methione is methionine sulphoxide"
XX
XX
XX US2002110851-A1.
XX
XX 15-AUG-2002.
XX
XX 02-MAR-2001; 2001US-00798116.
XX
XX 02-MAR-2000; 2000AU-00005995.
XX
XX (HALF-) HALT INST MEDICAL RES WALTER & ELITZA.
XX
XX Verhagen AM, Ekert PG, Vaux DL;
XX
XX WPI; 2003-074681/07.
XX
XX
XX New pro-apoptotic polypeptide, useful for screening for agents which
XX modulate cell death and for treating conditions associated with cell
XX death or apoptosis e.g. cancer.
XX
XX
XX Example 8; Page 4; 50pp; English.
XX
XX The invention relates to an isolated pro-apoptotic polypeptide,
XX designated DIABLO, or its biologically active fragment of 8 amino acids
XX in length. Also included are the polynucleotide encoding DIABLO,
XX expression vectors, transformed host cells, producing a biologically
XX active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP)
XX with a fragment of the polypeptide, and detecting a reduction in activity
XX of the IAP), producing a natural or synthetic variant of DIABLO with cell
XX death activity or which reduces IAP activity, an antigen- binding

CC molecule that specifically binds to DIABLO or its fragment, detecting
CC DIABLO in a biological sample (by contacting the sample with an IAP and
CC detecting the presence of an IAP/DIABLO complex), modulating the death of
CC a cell (by contacting a cell with an agent, which modulates the level
CC and/or functional activity of a polypeptide), a composition for
CC treatment/prophylaxis of a DIABLO related condition comprising an agent
CC which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a
CC nucleic acid encoding DIABLO, is useful for screening for an agent which
CC modulates cell death. An antigen-binding molecule is useful for detecting
CC DIABLO in a biological sample. The agent which modulates the level and/or
CC functional activity of a polypeptide comprising mature or pro-human
CC DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a
CC condition associated with expression or activation of DIABLO, such as
CC cancer, vascular disease, hepatic disease, autoimmune disease and
CC neurodegenerative disease, tissue damage or muscular tissue damage
CC associated with heart attack, or hepatic tissue damage associated with a
CC liver disease. DIABLO is also useful for treatment and/or prophylaxis of
CC conditions associated with cell death or apoptosis. The present sequence
CC represents a partial peptide sequence from human DIABLO, identified by
CC protein sequencing of a protein (later identified as DIABLO) which co-
CC precipitates with the human IAP protein MIRA (not defined)
CC
SQ Sequence 17 AA;

Query Match 32.6%; Score 28; DB 6; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KEDLWELL 17
:|::|
Db 5 EDEWQVQVI 13

RESULT 12
ADY39273
ID ADY39273 standard; peptide; 17 AA.
XX
XX
XX ADY39273;
XX
XX 19-MAY-2005 (first entry)
XX
XX
XX Human zsi933-gamma peptide, SEQ ID 14.
XX
XX
XX Gastrointestinal-Gen.; Osteopathic; Metabolic; Endocrine-Gen.;
XX Nephroretropic; Hepatotropic; Respiratory-Gen.; Nootropic; Dermatological;
XX Gynecological; Vulnereary; Antinflammatory; Antimicrobial; Anti-HIV;
XX Antibacterial; Vitruidey; Cytostatic; Immunomodulatory; Immunostimulant;
XX Gene Therapy; zsi933; musculoskeletal disease; endocrine disease;
XX nutritional disorder; metabolic disorder; growth disorder; wound healing;
XX genitourinary disease; gynecology and obstetrics; renal disease;
XX pulmonary disease; degeneration; inflammation; infectious disease;
XX cancer.
XX
XX Homo sapiens.
XX
XX US2005048618-A1.
XX
XX 03-MAR-2005.
XX
XX 19-AUG-2004; 2004US-00921371.
XX
XX 11-MAY-2000; 2000US-0203300P.
XX
XX 10-MAY-2001; 2001US-00853253.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Jaspers SR, Shepard PO, Deisher TA, Bishop PD;
XX
XX WPI; 2005-195284/20.
XX
XX N-PSDB; ADY39272.
XX
XX New zsi933-like polypeptide, useful for treating a disease, e.g.
XX osteoporosis, obesity, dwarfism, wound healing, inflammation, infectious

PT disease, HIV, bacterial or viral infection, or cancer.
XX
XX Claim 5; SEQ ID NO 14; 34pp; English.
PS
XX The present invention relates to novel zsi933-like peptides (I), which
CC are produced by peptide cleavage from the C-terminal end of zsi933.
CC zsi933 has homology to motilin and has been found to be transcribed in
CC the gastrointestinal system. The zsi933-like peptides and coding
CC sequences are useful for modulating gastric contractility, nutrient
CC uptake, growth hormones, the secretion of digestive enzymes and hormones,
CC and/or secretion of enzymes and/or hormones in the pancreas. They are
CC also useful for treating diseases and conditions associated with bone
CC formation (e.g. osteoporosis), immunity, obesity and metabolic disorders,
CC dwarfism, wound healing, reproduction, as well as conditions associated
CC with stress, kidney and lung dysfunction, aging and elderly, including,
CC muscle strength, bone fragility and skin thickness, and neuroendocrine
CC activities such as sleep. They are also useful for treating inflammation,
CC diabetic gastroparesis, infectious disease, HIV, bacterial or viral
CC infection, or cancer, for improving vaccines, and for stimulating an
CC immune response. The present sequence is one such zsi933-like peptide of
CC the invention. This sequence corresponds to residues 101-117 of the full-
CC length sequence.
XX
XX Sequence 17 AA;
SQ
Query Match 32.6%; Score 28; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 10 EDLIME 15
Db 3 QDILME 8
RESULT 13
AEF38807
ID AEF38807 standard; peptide: 17 AA.
XX
XX AEF38807;
AC
XX 23-MAR-2006 (first entry)
DT
XX
XX E. coli LacI repressor hinge region SEQ ID NO 15.
DE
XX fusion protein; LacI repressor; reporter protein; DNA purification.
KW
XX Escherichia coli.
OS
XX WO2006003355-A1.
PN
XX 12-JAN-2006.
PD
XX 08-MAR-2005; 2005WO-GB000888.
PF
XX 03-JUL-2004; 2004GB-00014987.
PR
XX (UYAS-) UNIV ASTON.
PA
XX Hine AV, Darby RAJ;
PI
XX WPI; 2006-090395/09.
DR
XX Novel protein comprising LacI repressor peptide and a 3-20 linker peptide
PT sequence, useful for purifying DNA.
XX
XX Claim 6; SEQ ID NO 15; 72pp; English.
PS
XX This invention describes a novel protein construct comprising a LacI
CC repressor peptide and a His3-20 linker peptide sequence or a LacI
CC repressor peptide (AEF38804), its functional variant and a linker peptide
CC AEF38810) adapted to bind to support surface. The invention also
CC describes: a) a nucleic acid encoding the construct; b) a vector
CC comprising the nucleic acid and c) a kit comprising the construct in

CC lyophilized form and a support surface. The construct comprises a fusion
CC protein, in which the LacI repressor peptide is fused, and thus
CC functionally bound to the linker peptide. The LacI repressor peptide
CC comprises an NH 2-terminal headpiece (AEF38806), a hinge region
CC (AEF38807), an inducer binding domain (AEF38808), and a COOH-terminal
CC helix (AEF38809). The construct also comprises a reporter protein
CC (AEF38813). The product of the invention is useful for purifying DNA
CC comprising at least a region of lacO operator or its variant which
CC involves contacting DNA comprising a region of lacO operator sequence
CC with the construct to form a DNA/protein complex, attaching the
CC DNA/protein complex to a support surface, and eluting the DNA from the
CC DNA/protein complex. The DNA to be purified comprises a) at least one of
CC lacO1, lacO2, lacO3 sites, or its derivative or variant; b) is contained
CC in a plasmid or a crude cell lysate. The support surface is adapted to
CC bind to the construct and comprises a porous resin. Eluting is carried
CC out by washing the support to which the protein/DNA complex is attached,
CC with an allosteric inducer of the LacI repressor protein (e.g. isopropyl-
CC beta-D-thiogalactopyranoside or allolactose) in conjunction with salt.
CC The method further involves a washing step of the DNA/protein complex
CC prior to the elution from the support surface. The construct allows rapid
CC and effective isolation of highly pure DNA, and is cost effective. This
CC sequence represents the E. coli LacI repressor protein hinge region, used
CC to make the construct LacI-His6-GFP.
XX
XX Sequence 17 AA;
SQ
Query Match 32.6%; Score 28; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 2 VARSMGKEDL 12
Db 7 VAQQLAGKOSL 17
RESULT 14
AAW58715
ID AAW58715 standard; peptide: 17 AA.
XX
XX AAW58715;
AC
XX 17-SEP-1998 (first entry)
DT
XX
XX Tryptic 40 kD subunit CLMP peptide off PVDF #8.
DE
XX Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize;
KW interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying;
KW proliferation; cytotoxic T cell; transplantation; antibody.
XX
XX Homo sapiens.
OS
XX US5780597-A.
PN
XX 14-JUL-1998.
PD
XX 02-JUN-1995; 95US-00460061.
PF
XX 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 24-MAR-1992; 92US-00857023.
PR 02-MAR-1994; 94US-00205011.
XX (HOF) HOFFMANN LA ROCHE INC.
PA
XX Podlaski FJ, Stern AS, Gately MK, Pan YE, Hulmes JD;
PI Chizzonice RA, Gubler UA;
PI
XX WPI; 1998-413150/35.
DR
XX New antibodies to cytotoxic lymphocyte maturation factor - useful for
PT detecting, purifying, and/or blocking proliferation and activation of
PT cytotoxic T cells, such as in transplantation(s).

```

XX
PS Example 3; Col 23; 71pp; English.
XX
CC An isolated antibody has been developed which binds specifically to
CC cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF
CC induced proliferation by more than 50% in a CLMF dependent T cell growth
CC assay and/or inhibits binding of at least 60% of the factor to
CC phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL)
CC blasts as determined in a CLMF receptor binding assay. CLMF is a
CC heterodimeric protein having a molecular weight band of 75 kD, determined
CC by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC under non-reducing and/or reducing conditions, providing a first subunit
CC having a molecular weight band of 40 kD and a second subunit having a
CC molecular weight of 35 kD. The present sequence represents a tryptic 40
CC kD CLMF peptide off polyvinylidene difluoride (PVDF), from an example of
CC the present invention. The antibody can be used for the purification
CC and/or detection of CLMF. It is also used in therapeutic treatments which
CC require selective blocking of proliferation and activation of cytotoxic T
CC cells (CTLs) such as in transplantation
XX
SQ Sequence 17 AA;
XX
Query Match 31.4%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 9 KEDLIW 14
    |||
    |||
    |||
Db 1 KEDGIW 6
XX
RESULT 15
AAU78549
ID AAU78549 standard; peptide; 17 AA.
XX
AC AAU78549;
XX
DT 18-JUN-2002 (first entry)
XX
DE Scrambled human perlecan cell adhesion peptide.
XX
KM Perlecan; cell adhesion; extracellular matrix; adhesive polypeptide;
KM heparin sulphate proteoglycan; HSPG2; scaffold; bone; cartilage;
KM tissue damage; tissue repair; bone loss; tooth loss; gum disease;
KM cartilage defect; rheumatoid arthritis; osteoarthritis; ulcer.
XX
OS Synthetic.
XX
PN WO200218423-A1.
XX
PD 07-MAR-2002.
XX
PF 27-AUG-2001; 2001WO-US026640.
XX
PR 31-AUG-2000; 2000US-0229222P.
PR 01-AUG-2001; 2001US-0309209P.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Farach-Carson MC, Carson DD, Safran JB;
XX
WPI; 2002-304245/34.
XX
DR
XX
PT New polypeptides derived from the perlecan core protein, useful for
PT strong and selective cell adhesion, particularly as coating for scaffolds
PT for tissue repair, e.g. for treating tooth or cartilage defects, or
PT repairing damaged skin.
XX
PS Example 2; Page 18; 41pp; English.
XX
CC This invention relates to an adhesive polypeptide derived from domain IV
CC of the extracellular matrix protein perlecan. Perlecan is a heparin
CC sulphate proteoglycan and is also known as HSPG2. The polypeptide of the

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CC invention allows strong and selective cell adhesion and is useful as
CC coating for scaffolds; e.g. implantable tissue scaffolds. The polypeptide
CC may be coated on matrices implanted in damaged tissue (e.g. bone or
CC cartilage) to increase the adhesion of desirable biological materials to
CC the repair site. The scaffolds are useful for treating tooth and jaw
CC defects (e.g. in cases of trauma, bone loss, tooth loss or gum disease)
CC or cartilage defects (e.g. those that result from rheumatoid arthritis,
CC osteoarthritis or trauma), or to repair defects and damage in skin,
CC muscle and other soft tissue such as those that result from trauma, burns
CC or ulcers. The present sequence represents a peptide composed of the
CC scrambled sequence of human perlecan adhesion peptide. This peptide was
CC used as a control for cell adhesion assays in the examples of the method
XX
SQ Sequence 17 AA;
XX
Query Match 31.4%; Score 27; DB 5; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.6e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
OY 4 RSMGKEDLIW 14
    :|||
    :|||
    :|||
Db 3 KSVG--SLIW 11
XX
Search completed: June 13, 2006, 01:27:39
Job time : 198 secs

```

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 01:33:43 ; Search time 38 Seconds
(without alignments)
43.044 Million cell updates/sec

Title: US-10-612-162A-1

Perfect score: 86

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 218

Minimum DB seq length: 17
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	26.7	17	2 B61334	trypsin (EC 3.4.21
2	21	24.4	17	2 A61321	histone H4 - commo
3	21	24.4	17	2 B61321	histone H4 - chick
4	20	23.3	17	2 PH0778	T-cell receptor al
5	20	23.3	17	2 G85956	hypothetical prote
6	19	22.1	17	2 PH1789	T cell receptor al
7	19	22.1	17	2 B49255	T-cell receptor be
8	19	22.1	17	2 B59137	protein Pf3 - gol
9	18	20.9	17	1 A05168	conantokin G [vali
10	18	20.9	17	2 A61334	trypsin (EC 3.4.21
11	18	20.9	17	2 B44873	caldesmon - rabbit
12	18	20.9	17	2 A61019	17K basolateral pl
13	17	19.8	17	2 C37396	pollen allergen Fe
14	17	19.8	17	2 C30221	histone H2A.8 - ch
15	17	19.8	17	2 A49635	Golli-mbp - human
16	17	19.8	17	2 I42753	interferon alpha (
17	16	18.6	17	2 S66198	alcohol dehydrogen
18	16	18.6	17	2 PN0587	tyrosine 3-monooxy
19	16	18.6	17	2 I46151	histone H2AF - dog
20	16	18.6	17	2 JP0046	histosomal protein
21	16	18.6	17	2 S15754	actin 6 - soybean
22	16	18.6	17	2 A46582	ferredoxin-phi
23	16	18.6	17	2 S69164	ferredoxin al - ja
24	16	18.6	17	2 A46218	ubiquinol-cytochro
25	16	18.6	17	2 B53113	gingipain, 44K - p
26	16	18.6	17	2 I45826	histone H2AF - New
27	15	17.4	17	2 B49404	T-cell receptor be
28	15	17.4	17	2 I58087	tyandodin receptor
29	15	17.4	17	2 A34572	osteonectin - rat

30	15	17.4	17	2 S78756	ribosomal protein
31	15	17.4	17	2 PH1630	ig H chain V-D-J r
32	15	17.4	17	2 A61518	undifferentiated prote
33	15	17.4	17	2 A37823	dihydroliipoamide S
34	15	17.4	17	2 S10786	enamelin, 26K - bo
35	15	17.4	17	2 A54205	heterogeneous ribo
36	14	16.3	17	2 PA0004	plascocyanin - Ara
37	14	16.3	17	2 S18534	hypothetical prote
38	14	16.3	17	2 PH0082	neuroglial protein
39	14	16.3	17	2 PT0234	ig heavy chain CRD
40	14	16.3	17	2 PH1331	ig heavy chain DJ
41	14	16.3	17	2 PH1357	ig heavy chain DJ
42	14	16.3	17	2 PH1312	ig heavy chain DJ
43	14	16.3	17	2 PH1820	T cell receptor al
44	14	16.3	17	2 S57514	T cell receptor be
45	14	16.3	17	2 B36727	cytochrome c554 -

ALIGNMENTS

RESULT 1

B61334
trypsin (EC 3.4.21.4) 2 - starfish (Dermasterias imbricata) (fragment)
C/Species: Dermasterias imbricata
C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C/Accession: B61334
R/Estell, D.A.; Laskowski Jr., M.
Biochemistry 19, 124-131, 1980
A/Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the reacti
A/Reference number: A61334; MUID:60109692; PMID:7352972
A/Accession: B61334
A/Molecule type: protein
A/Residues: 1-17 <EST>
A/Cross-references: UNIPROT:Q7M432; UNIPARC:UPI0000175C3B
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match

Best Local Similarity 26.7%; Score 23; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGCKE 10
: |||||

Db 2 VGCKE 6

RESULT 2

A61321
histone H4 - common cuttlefish (fragment)
C/Species: Sepia officinalis (common cuttlefish)
C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C/Accession: A61321
R/Routers-Tyrou, D.; Martin-Ponthieu, A.; Sautiere, P.; Bissette, G.
FEBS Lett. 128, 195-200, 1981
A/Title: Acetylation of histone H4 in chicken erythrocyte and cuttle-fish testis chromatin
A/Reference number: A61321; MUID:81261219; PMID:7262310
A/Accession: A61321
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <WOL>
A/Cross-references: UNIPROT:Q7M3Z5; UNIPARC:UPI00001771C6
C/Superfamily: histone H4
C/Keywords: acetylated amino end; acetyllysine
F/1/Modified site: acetylated amino end (Ser) #status experimental
F/5,12,16/Binding site: acetyl (Lys) (covalent) (partial) #status experimental

Query Match

Best Local Similarity 24.4%; Score 21; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RSMGK 9
| ||||

Db 3 RKGK GK 8

RESULT 3

B61321

histone H4 - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 31-Dec-2004

C/Accession: B61321

R/Mouters-Tyrou, D.; Martin-Ponthieu, A.; Sautiere, P.; Biserte, G.

FEBS Lett. 128, 195-200, 1981

A/Title: Acetylation of histone H4 in chicken erythrocyte and cuttle-fish testis chromatin

A/Reference number: A61321; PMID:1261219; PMID:7262310

A/Accession: B61321

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 <MOU>

A/Cross-references: UNIPROT:P70081; UNIPARC:UPI00001771C6

C/Keywords: acetylated amino end; acetyllysine

F/1/Modified site: acetylated amino end (Ser) #status experimental

F/5.12.16/Binding site: acetyl (Lys) (covalent) (partial) #status experimental

Query Match 24.4%; Score 21; DB 2; Length 17;

Best Local Similarity 66.7%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RSMGK GK 9

Db 3 RKGK GK 8

RESULT 4

PH0778

T-cell receptor alpha chain (RA10.3.3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0778

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Marjanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-1

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; PMID:92078846; PMID:1836010

A/Accession: PH0778

A/Molecule type: mRNA

A/Residues: 1-17 <CNS>

A/Cross-references: UNIPARC:UPI000017C784; EMBL:X60875

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match 23.3%; Score 20; DB 2; Length 17;

Best Local Similarity 40.0%; Pred. No. 5.2e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 SMGKEDLIW 14

Db 7 NQGSAGKLIF 16

RESULT 5

G85956

hypothetical protein 24331 (imported) - Escherichia coli (strain O157:H7, substrain EDL93

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: G85956

R/Perna, N.T.; Plunkett II, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; PMID:21074935; PMID:11206551

A/Accession: G85956

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-17 <STO>

A/Cross-references: UNIPROT:Q8X4A4; UNIPARC:UPI000000DE1B; GB:AE005174; NID:g12517539; PJ
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: 24331

Query Match 23.3%; Score 20; DB 2; Length 17;

Best Local Similarity 57.1%; Pred. No. 5.2e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GSKEDLI 13

Db 9 GSKYGLD 15

RESULT 6

PH1789

T cell receptor alpha chain V region (clone 2PBL V alpha 24-5) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1789

R/porcelli, S.; Fockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; PMID:93301585; PMID:8391057

A/Accession: PH1789

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-17 <POR>

A/Cross-references: UNIPARC:UPI000017C378

Query Match 22.1%; Score 19; DB 2; Length 17;

Best Local Similarity 38.5%; Pred. No. 7.7e+03;

Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 VARSMGKEDLIW 14

Db 4 VVPSGSGYNKLIF 16

RESULT 7

B49255

T-cell receptor beta chain V-D-J-C region (V beta 8, J beta 2.7) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C/Accession: B49255

R/Rosenberg, W.M.; Mose, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A/Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A/Reference number: A49039; PMID:92164737; PMID:1311263

A/Accession: B49255

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-17 <ROS>

A/Cross-references: UNIPARC:UPI000017C3BA

A/Note: sequence extracted from NCBI backbone (NCBI:P.90723)

C/Keywords: T-cell receptor

Query Match 22.1%; Score 19; DB 2; Length 17;

Best Local Similarity 60.0%; Pred. No. 7.7e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSKED 11

Db 9 GGRHE 13

RESULT 8

E59137

protein pfd3 - golden needle mushroom (fragment)

C/Species: Flammulina velutipes (golden needle mushroom)

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: E59137

R;Sakamoto, Y.; Ando, A.; Tama, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A;Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A;Reference number: A59137
A;Accession: E59137
A;Molecule type: protein
A;Residues: 1-17 <SAK>
A;Cross-references: UNIPROT:Q7M4W7, UNIPARC:UPI000017CB26

Query Match 22.1%; Score 19; DB 2; Length 17;
Best Local Similarity 28.6%; Pred. No. 7.7e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 11 DLWELL 17
| : | :
Db 5 DVYWHV 11

RESULT 9
A05168
conantokin G (validated) - cone shell (Conus geographus)
N/Alternate names: conotoxin GV, sleeper peptide
C;Species: Conus geographus (Geography cone)
C;Date: 10-Sep-1989 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A05168
R;McIntosh, J.M.; Oliveira, B.M.; Cruz, L.J.; Gray, W.R.
J. Biol. Chem. 259, 14343-14346, 1984
A;Title: gamma-Carboxyglutamate in a neuroactive toxin.
A;Reference number: A05168; MUID:85054897; PMID:6501296
A;Accession: A05168
A;Molecule type: protein
A;Residues: 1-17 <MCI>
A;Cross-references: UNIPROT:P07231, UNIPARC:UPI000014A469
R;Rigby, A.C.; Baleja, J.D.; Furie, B.C.; Furie, B.
submitted to the Brookhaven Protein Data Bank, February 1997
A;Reference number: A67471; PDB:1AD7
A;Contents: annotation; conformation by (1)H-NMR, residues 1-17
R;Rigby, A.C.; Baleja, J.D.; Furie, B.C.; Furie, B.
Biochemistry 36, 6906-6914, 1997
A;Title: Three-dimensional structure of a gamma-carboxyglutamic acid-containing conotoxi
A;Reference number: A58650; MUID:97332451; PMID:918685
A;Contents: annotation; conformation by (1)H-NMR
C;Superfamily: conantokin
C;Keywords: amidated carboxyl end; carboxyglutamic acid; neurotoxin; venom
F;3,4,7,10,14/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F;17/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 20.9%; Score 18; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 8 GKEDL 12
| : | :
Db 1 GEEEL 5

RESULT 10
A61334
crypsin (EC 3.4.21.4) 1 - starfish (Dermasterias imbricata) (fragment)
C;Species: Dermasterias imbricata
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C;Accession: A61334
R;Bastell, D.A.; Laskowski Jr., M.
Biochemistry 19, 124-131, 1980
A;Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the reacti
A;Reference number: A61334; MUID:80109692; PMID:7352972
A;Accession: A61334
A;Molecule type: protein
A;Residues: 1-17 <EST>
A;Cross-references: UNIPROT:Q7M433; UNIPARC:UPI0000175C3A
C;Comment: This isoform is novel in that it readily dissociates from bovine pancreatic tr
inhibited.
C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 20.9%; Score 18; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 6 MGKEDL 12
| : | :
Db 2 VGGHEV 8

RESULT 11
B44873
caldesmon - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B44873
R;Ikeda, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei
A;Reference number: A44873; MUID:91378498; PMID:1898046
A;Accession: B44873
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <IKI>
A;Cross-references: UNIPROT:Q9TRW1; UNIPARC:UPI0000086A69
A;Experimental source: skeletal myosin
A;Note: sequence extracted from NCBI backbone (NCBIP:63202)
C;Superfamily: caldesmon

Query Match 20.9%; Score 18; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 13 IWE 15
| : | :
Db 2 LWE 4

RESULT 12
A61019
17K basolateral plasma membrane protein Procl7 - rat (fragment)
N/Alternate names: Procl7
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994
C;Accession: A61019
R;Schlecht, H.
Histochemistry 93, 513-518, 1990
A;Title: N-terminal amino acid sequence, immunohistochemical localization and tissue dis
A;Reference number: A61019; MUID:90236771; PMID:2332352
A;Accession: A61019
A;Molecule type: protein
A;Residues: 1-17 <SCH>
A;Cross-references: UNIPARC:UPI000017C89C
C;Keywords: intestine; membrane protein

Query Match 20.9%; Score 18; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GGGK 10
| : | :
Db 12 GGGK 15

RESULT 13
C37396
pollen allergen Fes e I type A - reed fescue (fragment)
C;Species: Festuca elatior (reed fescue)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 25-Oct-1996
C;Accession: C37396
R;Esch, R.E.; Klapper, D.G.
Mol. Immunol. 26, 557-561, 1989

A>Title: Isolation and characterization of a major cross-reactive grass group I allergen
A/Reference number: A37396; MUID:89364850; PMID:2475768
A/Accession: C37396
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <ESCC>
A/Cross-references: UNIPARC:UPI000017B0DA
C/Keywords: pollen

Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EDLWE 15
||:|
Db 12 EDVPE 17

RESULT 14

C30221 histone H2A.8 - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 02-Nov-1989 #sequence_revision 02-Nov-1989 #text_change 30-Sep-1993
C/Accession: C30221
R/Challoner, P.B.; Moss, S.B.; Groudine, M.
Mol. Cell. Biol. 9, 902-913, 1989
A/Title: Expression of replication-dependent histone genes in avian spermatids involves
A/Reference number: A30221; MUID:89261754; PMID:2471062
A/Accession: C30221
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-17 <CHA>
A/Cross-references: UNIPARC:UPI000017C00F

Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSK 9
||
Db 8 GSK 10

RESULT 15

A49635 GO111-mbp - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Nov-1999
C/Accession: A49635
R/Pridyl, T.M.; Campagnoni, C.W.; Kampf, K.; Kaehina, T.; Handley, V.W.; McMahon, J.; Ca
Proc. Natl. Acad. Sci. U.S.A. 90, 10695-10699, 1993
A/Title: The human myelin basic protein gene is included within a 179-kilobase transcrip
A/Reference number: A49635; MUID:94068468; PMID:7504278
A/Accession: A49635
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-17 <RES>
A/Cross-references: UNIPARC:UPI000016AFAB; GB:L18862; NID:g435054; PIDN:AAA72008.1; PID:

Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 GKEDL 12
||:|
Db 6 GKREL 10

Search completed: June 13, 2006, 01:44:16
Job time : 39 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 01:24:33 ; Search time 291 Seconds
(without alignments)
54.039 Million cell updates/sec

Title: US-10-612-162A-1
Perfect score: 86
Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 1270

Minimum DB seq length: 17
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	33.7	17	2	Q6LDL9_RAT
2	29	33.7	17	2	Q6LEA8_XENLA
3	23	26.7	17	2	Q7M432_DERIM
4	23	26.7	17	2	Q9R4A5_OERXA
5	22	25.6	17	1	PH4_PBRAM
6	22	25.6	17	2	Q85AH6_PPRIM
7	22	25.6	17	2	Q85AH7_HAPGR
8	22	25.6	17	2	Q85DA2_GALSE
9	22	25.6	17	2	Q85DA6_GALCR
10	22	25.6	17	2	Q85DB4_LEPRU
11	22	25.6	17	2	Q8HB37_VARVV
12	22	25.6	17	2	Q8HB38_VARVV
13	22	25.6	17	2	Q8HB39_HAPSI
14	22	25.6	17	2	Q8HB40_HAPGR
15	22	25.6	17	2	Q8HB41_HAPGR
16	22	25.6	17	2	Q8HOB0_HAPGR
17	22	25.6	17	2	Q94NE1_EULMO
18	22	25.6	17	2	Q94NE2_MICRF
19	22	25.6	17	2	Q94NE3_MIRCO
20	22	25.6	17	2	Q94NE5_CHEMA
21	22	25.6	17	2	Q94NE6_CHEME
22	22	25.6	17	2	Q94XZ3_EULRU
23	22	25.6	17	2	Q94XZ7_EULCO
24	22	25.6	17	2	Q94Y89_LEMCA
25	22	25.6	17	2	Q955R8_DNUMA
26	22	25.6	17	2	Q955T6_ALUTR
27	22	25.6	17	2	Q9B0V8_PROVE
28	22	25.6	17	2	Q9B0V9_PROVE
29	22	25.6	17	2	Q9B0W0_PROVE
30	22	25.6	17	2	Q9B0W1_PROVE
31	22	25.6	17	2	Q9B8T3_PROTA

32	22	25.6	17	2	Q9B8T7_PPRIM	Q9B8T7 propithecus
33	22	25.6	17	2	Q9B8U1_AVALA	Q9B8U1 avahi lang
34	22	25.6	17	2	Q9G116_PPRIM	Q9G116 eulemur ful
35	22	25.6	17	2	Q9G117_PPRIM	Q9G117 eulemur ful
36	22	25.6	17	2	Q9G118_EULFC	Q9G118 eulemur ful
37	22	25.6	17	2	Q9G119_PPRIM	Q9G119 eulemur ful
38	22	25.6	17	2	Q9G120_PPRIM	Q9G120 eulemur ful
39	22	25.6	17	2	Q9G121_PPRIM	Q9G121 eulemur ful
40	22	25.6	17	2	Q9G122_EULFU	Q9G122 eulemur ful
41	22	25.6	17	2	Q9G5F8_EULMF	Q9G5F8 eulemur mac
42	22	25.6	17	2	Q9GA08_EULMF	Q9GA08 eulemur mac
43	22	25.6	17	2	Q94NE3_MICRA	Q94NE3 microcebus
44	22	25.6	17	2	Q9APR4_PSEAE	Q9APR4 pseudomnas
45	22	25.6	17	2	Q69074_HHVI	Q69074 human herpe

ALIGNMENTS

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RESULT 1
Q6LDL9_RAT PRELIMINARY; PRT; 17 AA.
AC Q6LDL9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "transcription initiation sites and structural organization of the
RL Mo. Cell. Biol. 10:3314-3324(1990).
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CC -----
DR EMBL; M32612; AAA41680.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 17 AA; 2026 MW; AEA1EBSF52E84F5 CRC64;

Query Match 33.7%; Score 29; DB 2; Length 17;
Best local similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EDLIWEL 16
Db 5 KDLIWL 11

RESULT 2
Q6LEA8_XENLA PRELIMINARY; PRT; 17 AA.
AC Q6LEA8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 5.
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RA Johnson A.D., Ovesnek N., Tonissen K.F., Krieg P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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DR EMBL, L26396; AAA4911.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 33.7%; Score 29; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 1,7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EDLWEL 16
DB 5 KDILWTL 11

RESULT 3
ID Q7M432.DERIM PRELIMINARY; PRT; 17 AA.
AC Q7M432;
DT 15-DEC-2003, integrated into UniProtKB/TREMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 6.
OS Trypsin (EC 3.4.21.4) 2 (Fragment).
OC Dermasterias imbricata (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asteriinae; Dermasterias.
OC NCBI_TaxID=7590;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=60109692; PubMed=7352972;
RA Batell D.A., Laszkowski Jr., M.;
RT "Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes
RT the reactive-site peptide bonds of protein trypsin inhibitors.";
RL Biochemistry 19:124-131(1980).
CC -----
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CC -----
DR PIR; B61334; B61334.
DR GO; GO:0004295; F:trypsin activity; IEA.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1800 MW; 4C7B64410B84D968 CRC64;

Query Match 26.7%; Score 23; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGSGKE 10
DB 2 VGSKE 6

RESULT 4
ID Q9R4A5.OERXA PRELIMINARY; PRT; 17 AA.
AC Q9R4A5;
DT 01-MAY-2000, integrated into UniProtKB/TREMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Lytic beta-1,3-glucanase (Fragment).
OS Oerskovia xanthoneolytica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccinae; Promicromonosporaceae; Cellulosimicrobium.
OC NCBI_TaxID=1710;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96250169; PubMed=8659924;
```

```
RA Ferrer P., Hedegaard L., Halkier T., Diere I., Savva D., Aeenjo U.A.;
RT "Molecular cloning of a lytic beta-1,3-glucanase gene from Oerskovia
RT xanthoneolytica L66109. A beta-1,3-glucanase able to selectively
RT permeabilize the yeast cell wall.";
RL Ann. N. Y. Acad. Sci. 782:555-565(1996).
CC -----
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CC -----
SQ SEQUENCE 17 AA; 1708 MW; 0CAD9148FA52A15 CRC64;

Query Match 26.7%; Score 23; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLWEL 14
DB 4 DPLWQL 7

RESULT 5
ID PH4.PERAM STANDARD; PRT; 17 AA.
AC P82697;
DT 04-MAY-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 21.
DE Peptide hormone 4 (Pea-YUS-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
OC NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20140865; PubMed=10676456;
RA Predel R., Eckert M., Holman G.M.;
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
RT of insects.";
RL Ann. N. Y. Acad. Sci. 897:282-290(1999).
CC -1- FUNCTION: Unknown.
CC -1- MASS SPECTROMETRY: MW=1966.48; METHOD=MALDI; RANGE=1-17;
CC NOTE=Ref.1.
CC -----
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CC -----
KM Annotation: Direct protein sequencing; Neuropeptide.
FT PEPTIDE 1 17
FT MOD_RES 17 17 Peptide hormone 4.
FT FTID=PRO.0000044205. Serine amide.
SQ SEQUENCE 17 AA; 1968 MW; CAAFB57ECD8218A9 CRC64;

Query Match 25.6%; Score 22; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLWEL 16
DB 2 DPLWQL 7

RESULT 6
ID Q85AH6.9PRIM PRELIMINARY; PRT; 17 AA.
AC Q85AH6;
DT 01-JUN-2003, integrated into UniProtKB/TREMBL.
DT 01-JUN-2003, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).
```



```
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Euarchontoglires; Primates; Strepsirrhini;
OC Megaladapidae; Lepilemur.
OX NCBI_TaxID=122230;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Paetorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
CC -----
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CC -----
DR EMBL; AF224593; AAP33636.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000298; Cytc_oxdse_III.
DR PANTHER; PTHR11403; Cytc_oxdse_III; 1.
DR Pfam; PF00510; COX3; 1.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2132 MW; CBBE69E354D98978 CRC64;

Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 11 DLIELL 17
|:|
Db 2 DVVWLF 8

RESULT 7
085AH7 HAPGR PRELIMINARY; PRT; 17 AA.
AC 085AH7
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Hapalemur griseus alaotrensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnidae; Hapalemur.
OX NCBI_TaxID=122220;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Paetorini J., Forstner M.R.J., Martin R.D.;
RT "Phylogenetic relationships of gentle lemurs (Hapalemur).";
RL Evol. Anthropol. 11:150-154(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Paetorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
CC -----
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CC -----
DR EMBL; AF224575; AAO37906.1; -; Genomic DNA.
DR EMBL; AF224576; AAO37910.1; -; Genomic DNA.
DR EMBL; AF224577; AAO37914.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
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DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000298; Cytc_oxdse_III.
DR PANTHER; PTHR11403; Cytc_oxdse_III; 1.
DR Pfam; PF00510; COX3; 1.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2132 MW; CBBE69E354D98978 CRC64;

Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 11 DLIELL 17
|:|
Db 2 DVVWLF 8

RESULT 8
085DA2 GALSE PRELIMINARY; PRT; 17 AA.
AC 085DA2
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Galago senegalensis (Northern lesser bushbaby).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Euarchontoglires; Primates; Strepsirrhini;
OC Galagonidae; Galago.
OX NCBI_TaxID=9465;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Paetorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
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CC -----
DR EMBL; AF224644; AAP33660.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000298; Cytc_oxdse_III.
DR PANTHER; PTHR11403; Cytc_oxdse_III; 1.
DR Pfam; PF00510; COX3; 1.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2132 MW; CBBE69E354D98978 CRC64;

Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 11 DLIELL 17
|:|
Db 2 DVVWLF 8

RESULT 9
085DA6 GALCR PRELIMINARY; PRT; 17 AA.
AC 085DA6
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 11.
DT 07-FEB-2006, entry version 11.
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DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Galagonidae; Otolemur.
OX NCBI_TaxID=9463;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
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CC -----
DE EMBL: AF224596; AAP33648.1; -; Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000298; CytoC_oxide_III; 1.
DR PANTHER: PTHR11403; CytoC_oxide_III; 1.
DR Pfam: PF00510; COX3; 1.
KW Mitochondrion.
SQ SEQUENCE 17 AA; 2132 MW; CBBB69E354D98978 CRC64;
FT NON_TER 1
QY 11 DLIWELL 17
Db 2 DVMWLF 8

RESULT 10
Q85DB4_LEPRU PRELIMINARY; PRT; 17 AA.
AC Q85DB4;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Lepilemur ruficaudatus (Red-tailed sportive lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Megaladapidae; Lepilemur.
OX NCBI_TaxID=78866;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
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CC -----
DE EMBL: AF224596; AAP33648.1; -; Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000298; CytoC_oxide_III; 1.
DR PANTHER: PTHR11403; CytoC_oxide_III; 1.
DR Pfam: PF00510; COX3; 1.
KW Mitochondrion.
SQ SEQUENCE 17 AA; 2132 MW; CBBB69E354D98978 CRC64;
FT NON_TER 1
QY 11 DLIWELL 17
Db 2 DVMWLF 8

Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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DR Pfam: PF00510; COX3; 1.
KW Mitochondrion.
SQ SEQUENCE 17 AA; 2132 MW; CBBB69E354D98978 CRC64;
FT NON_TER 1
QY 11 DLIWELL 17
Db 2 DVMWLF 8

RESULT 11
Q8HB37_VARVV PRELIMINARY; PRT; 17 AA.
AC Q8HB37;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Varecia variegata variegata (Black and white ruffed lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnidae; Varecia.
OX NCBI_TaxID=87289;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22281620; PubMed=12393004; DOI=10.1016/S0047-2484(02)90587-7;
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships among Lemnidae (Primates): evidence from
mtDNA."
RL J. Hum. Evol. 43:463-478 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships of gentle lemurs (Haplemur).";
RL Evol. Anthropol. 11:150-154 (2002).
CC -----
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CC -----
DE EMBL: AF224585; AAN64789.1; -; Genomic_DNA.
DR EMBL: AF224586; AAN64793.1; -; Genomic_DNA.
DR EMBL: AF224587; AAN64797.1; -; Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000298; CytoC_oxide_III; 1.
DR PANTHER: PTHR11403; CytoC_oxide_III; 1.
DR Pfam: PF00510; COX3; 1.
KW Mitochondrion.
SQ SEQUENCE 17 AA; 2132 MW; CBBB69E354D98978 CRC64;
FT NON_TER 1
QY 11 DLIWELL 17
Db 2 DVMWLF 8

Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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RESULT 12
Q8HB38_VARVR PRELIMINARY; PRT; 17 AA.
ID Q8HB38
AC Q8HB38
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 13.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Varecia variegata rubra (Red ruffed lemur).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnidae; Varecia.
OX NCBI_TaxID=30604;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22281620; PubMed=12393004; DOI=10.1016/S0047-2484(02)90587-7;
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships of gentle lemurs (Haplemur).";
RL Evol. Anthropol. 11:150-154(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
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DR EMBL; AF224588; AAN64801.1 -; Genomic_DNA.
DR EMBL; AF224589; AAN64805.1 -; Genomic_DNA.
DR EMBL; AF224591; AAN64813.1 -; Genomic_DNA.
DR EMBL; AF224590; AAN64809.1 -; Genomic_DNA.
DR EMBL; AF224592; AAN64817.1 -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000298; Cytochrome_c_oxidase_subunit_III.
DR PANTHER; PTHR11403; Cytochrome_c_oxidase_subunit_III; 1.
DR Pfam; PF00510; COX3; 1.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 17 AA; 2132 MW; CBBE69E354D98978 CRC64;

Query March 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 DLIELL 17
Db 2 DVVWLF 8

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GN Name=COIII;
OS Haplemur simus (Greater bamboo lemur).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnidae; Haplemur.
OX NCBI_TaxID=122223;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22281620; PubMed=12393004; DOI=10.1016/S0047-2484(02)90587-7;
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from
mtDNA.";
RL J. Hum. Evol. 43:463-478(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pastorini J., Forstner M.R.J., Martin R.D.;
RT "Phylogenetic relationships of gentle lemurs (Haplemur).";
RL Evol. Anthropol. 11:150-154(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
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DR Pfam; PF00510; COX3; 1.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 17 AA; 2132 MW; CBBE69E354D98978 CRC64;

Query March 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 DLIELL 17
Db 2 DVVWLF 8

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RESULT 13
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ID Q8HB39
AC Q8HB39
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Cytochrome oxidase subunit III (Fragment).

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ID Q8HB40
AC Q8HB40
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Haplemur griseus occidentalis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnidae; Haplemur.
OX NCBI_TaxID=122221;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22281620; PubMed=12393004; DOI=10.1016/S0047-2484(02)90587-7;
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from
mtDNA.";

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RL J. Hum. Evol. 43:463-478(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pastorini J., Forester M.R.J., Martin R.D.;
RT "Phylogenetic relationships of gentle lemurs (Hapalemur).";
RL Evol. Anthropol. 11:150-154(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; Pubmed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalman U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
CC
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DR EMBL: AF224578; AAN64765.1; -; Genomic DNA.
DR EMBL: AF224579; AAN64769.1; -; Genomic DNA.
DR EMBL: AF224580; AAO37918.1; -; Genomic DNA.
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DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000298; Cytc_oxdase_III.
DR PANTHER: PTHR11403; Cytc_oxdase_III; 1.
DR Pfam: PF00510; COX3; 1.
DR Mitochondrion.
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Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 11 DLIMELL 17
Db 2 DVMWFL 8
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AC Q8HB41;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Hapalemur aureus (golden bamboo lemur).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini;
OC Lemnidae; Hapalemur.
OX NCBI_TaxID=122222;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2281620; Pubmed=12393004; DOI=10.1016/S0047-2484(02)90587-7;
RA Pastorini J., Forester M.R., Martin R.D.;
RT "Phylogenetic relationships among Lemnidae (Primates): evidence from
mtDNA.";
RL J. Hum. Evol. 43:463-478(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pastorini J., Forester M.R.J., Martin R.D.;
RT "Phylogenetic relationships of gentle lemurs (Hapalemur).";
RL Evol. Anthropol. 11:150-154(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631663; Pubmed=12719521; DOI=10.1073/pnas.1031673100;
RA Pastorini J., Thalman U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
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RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
CC
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DR EMBL: AF224581; AAN64773.1; -; Genomic DNA.
DR EMBL: AF224582; AAN64777.1; -; Genomic DNA.
DR GO: GO:0016020; C:membrane; IEA.
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DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000298; Cytc_oxdase_III.
DR PANTHER: PTHR11403; Cytc_oxdase_III; 1.
DR Pfam: PF00510; COX3; 1.
DR Mitochondrion.
KW NON_TER
FT SEQUENCE 17 AA; 2132 MW; CBBB69E354D98978 CRC64;
SQ
Query Match 25.6%; Score 22; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 11 DLIMELL 17
Db 2 DVMWFL 8
Search completed: June 13, 2006, 01:32:34
Job time : 293 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 01:43:53 ; Search time 48 Seconds
(without alignments)
31.000 Million cell updates/sec

Title: US-10-612-162A-1
Perfect score: 86
Sequence: 1 VVARSMGCKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 6669

Minimum DB seq length: 17
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /EMC_Celerra_SIDS3/ptocdata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SIDS3/ptocdata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SIDS3/ptocdata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/ptocdata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/ptocdata/2/iaa/PCMS.COMB.pep.*
6: /EMC_Celerra_SIDS3/ptocdata/2/iaa/RS.COMB.pep.*
7: /EMC_Celerra_SIDS3/ptocdata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	32.6	17	2	US-09-853-253-14
2	26	30.2	17	1	US-08-497-599-5
3	26	30.2	17	2	US-09-564-677A-18
4	25	29.1	17	2	US-09-845-160-4
5	24.5	28.5	17	2	US-09-695-437A-40
6	24	27.9	17	2	US-09-025-769B-229
7	24	27.9	17	2	US-09-490-070A-229
8	24	27.9	17	2	US-09-490-153-229
9	24	27.9	17	2	US-09-490-324-229
10	23.5	27.3	17	2	US-08-635-928-32
11	23.5	27.3	17	2	US-08-635-928-33
12	23	26.7	17	1	US-08-333-565-14
13	23	26.7	17	1	US-08-382-013A-9
14	23	26.7	17	1	US-08-321-625-52
15	23	26.7	17	1	US-08-661-479-14
16	23	26.7	17	1	US-08-497-599-4
17	23	26.7	17	2	US-09-192-048-16
18	23	26.7	17	2	US-09-195-666A-21
19	23	26.7	17	2	US-09-181-083-52
20	23	26.7	17	2	US-09-635-705-21
21	23	26.7	17	2	US-09-634-858A-21
22	23	26.7	17	2	US-08-869-927C-21
23	23	26.7	17	2	US-09-750-754-52
24	23	26.7	17	2	US-09-779-333-2
25	22	25.6	17	1	US-07-702-771-3
26	22	25.6	17	1	US-08-335-303-58

27	22	25.6	17	1	US-08-241-054-116	Sequence 116, App
28	22	25.6	17	1	US-08-370-567-14	Sequence 14, Appl
29	22	25.6	17	1	US-08-438-759-14	Sequence 14, Appl
30	22	25.6	17	1	US-08-704-170-24	Sequence 24, Appl
31	22	25.6	17	1	US-08-438-883-3	Sequence 3, Appl
32	22	25.6	17	1	US-08-741-599-3	Sequence 3, Appl
33	22	25.6	17	1	US-08-485-508-116	Sequence 116, App
34	22	25.6	17	1	US-08-497-599-13	Sequence 13, Appl
35	22	25.6	17	1	US-08-751-305-18	Sequence 18, Appl
36	22	25.6	17	2	US-08-753-750B-55	Sequence 55, Appl
37	22	25.6	17	2	US-09-428-082B-204	Sequence 204, App
38	22	25.6	17	5	PCT-US91-05177-2	Sequence 2, Appl
39	22	25.6	17	5	PCT-US94-02631-24	Sequence 24, Appl
40	22	25.6	17	5	PCT-US94-05684-14	Sequence 14, Appl
41	22	25.6	17	7	5266328-7	Patent No. 5266328
42	21	24.4	17	1	US-08-076-092-10	Sequence 10, Appl
43	21	24.4	17	1	US-08-105-416-29	Sequence 29, Appl
44	21	24.4	17	1	US-08-569-188-4	Sequence 4, Appl
45	21	24.4	17	1	US-08-569-188-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-853-253-14
Sequence 14, Application US/09853253
Patent No. 6897286
GENERAL INFORMATION:
APPLICANT: JASPER, STEPHEN
APPLICANT: SHEPPARD, PAUL
APPLICANT: BISHOP, PAUL
APPLICANT: DIESHER, THERESA
TITLE OF INVENTION: Zeig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-253-14

Query Match 32.6%; Score 28; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 10 EDLWE 15
3 QDIME 8

RESULT 2
US-08-497-599-5
Sequence 5, Application US/08497599
Patent No. 5808828
GENERAL INFORMATION:
APPLICANT: Kurita, Takashi
APPLICANT: Matsumoto, Tomoaki
APPLICANT: Kikuno, Reiko
APPLICANT: Otawara-Hamamoto, Yoko
APPLICANT: Breidohl, Gerhard
TITLE OF INVENTION: Synthetic Peptide Derivatives And The
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I. Street, N.W., Suite 700

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,599
FILING DATE: 30-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Toohy, Kimberlin M.
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1451-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-497-599-5

Query Match 30.2%; Score 26; DB 1; Length 17;
Best Local Similarity 28.6%; Pred. No. 7.5e+02;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 9 KEDLWE 15
DB 3 RQDILWK 9

RESULT 3
US-09-564-677A-18
Sequence 18, Application US/09564677A
Patent No. 6664368
GENERAL INFORMATION:
APPLICANT: Asgaf Friedler
APPLICANT: Abraham Loyler
APPLICANT: Chaim Gilon
APPLICANT: Amnon Wolf
TITLE OF INVENTION: Inhibition of Nuclear Import by Backbone Cyclic Peptide Analogs
FILE REFERENCE: 2254-019-999
CURRENT APPLICATION NUMBER: US/09/564,677A
CURRENT FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 122343
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: PCT/IL98/00577
PRIOR FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FaatSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 17
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus (HIV-1)
US-09-564-677A-18

Query Match 30.2%; Score 26; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RSWG 8
DB 3 RSWG 7

RESULT 4

US-09-845-160-4
Sequence 4, Application US/09845160
Patent No. 6921663
GENERAL INFORMATION:
APPLICANT: MIZUGUCHI, HIROYUKI
APPLICANT: HAYAKAWA, TAKAO
TITLE OF INVENTION: ADENOVIRUS VECTOR
FILE REFERENCE: 081356/0163
CURRENT APPLICATION NUMBER: US/09/845,160
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: JP 2001-131688
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: JP 2000-161577
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide having affinity with E-selectin.
US-09-845-160-4

Query Match 29.1%; Score 25; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLIEWL 17
DB 8 DQWMDM 14

RESULT 5
US-09-695-437A-40
Sequence 40, Application US/09695437A
Patent No. 6803203
GENERAL INFORMATION:
APPLICANT: Brookhaven Science Associates
APPLICANT: Anderson, Carl W
APPLICANT: Connolly, Margery A
TITLE OF INVENTION: DNA-PK Assay
FILE REFERENCE: BSA 01-02
CURRENT APPLICATION NUMBER: US/09/695,437A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/398,139
PRIOR FILING DATE: 1995-03-03
PRIOR APPLICATION NUMBER: 08/132,284
PRIOR FILING DATE: 1993-10-06
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Version 3.1
SEQ ID NO 40
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)-(4)
OTHER INFORMATION: human hsp90 residues 1-4
NAME/KEY: MISC_FEATURE
LOCATION: (5)-(17)
OTHER INFORMATION: human p53 residues 15-27 with S20S substitution
US-09-695-437A-40

Query Match 28.5%; Score 24.5; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 10 EDLIEWL 17
DB 10 EDL-WKLL 16

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RESULT 6
US-09-025-769B-229
; Sequence 229, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 229:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-025-769B-229

Query Match      27.9%; Score 24; DB 2; Length 17;
Best Local Similarity 43.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY      3 ARSM---GKEDLIW 14
Db      2 ARNMALSRGKMDVW 17

RESULT 7
US-09-490-070A-229
; Sequence 229, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
```

```
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 229:

US-09-490-070A-229

Query Match      27.9%; Score 24; DB 2; Length 17;
Best Local Similarity 43.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY      3 ARSM---GKEDLIW 14
Db      2 ARNMALSRGKMDVW 17

RESULT 8
US-09-490-153-229
; Sequence 229, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 229:
US-09-490-153-229

Query Match 27.9%; Score 24; DB 2; Length 17;
Best local Similarity 43.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 3 ARSM---GGKEDLIW 14
||:| |||:|
Db 2 ARNMALSRGKENDVW 17

RESULT 9
US-09-490-324-229
Sequence 229, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 229:
US-09-490-324-229

Query Match 27.9%; Score 24; DB 2; Length 17;
Best local Similarity 43.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 3 ARSM---GGKEDLIW 14
||:| |||:|
Db 2 ARNMALSRGKENDVW 17

RESULT 10
US-08-635-928-32
Sequence 32, Application US/08635928
Patent No. 6291639
GENERAL INFORMATION:
APPLICANT: CONRAD, JURGEN
APPLICANT: DINKELBORG, LUDGER
APPLICANT: ERBER, SEBASTIAN
APPLICANT: FROMMEL, CORNELIUS
APPLICANT: HOFNE, WOLFGANG
APPLICANT: KRAMP, WOLFGANG
APPLICANT: KUTTNER, GABRIELE
APPLICANT: MALIN, REINHARD
APPLICANT: SCHIER, HANS MARTIN
APPLICANT: SCHNEIDER-MERGENER, JENS
TITLE OF INVENTION: METAL-BINDING CYSTEIN-FREE
TITLE OF INVENTION: PEPTIDES FOR DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTICAL PURPOSES,
TITLE OF INVENTION: METHODS FOR THEIR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY LLP
STREET: Four Embarcadero Center, Suite 400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,928
FILING DATE: 09/20/96
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE94/01302
FILING DATE: 10/27/94
APPLICATION NUMBER: P4337599.5
FILING DATE: 11/01/93
ATTORNEY/AGENT INFORMATION:
NAME: Molano, Michael A.
REGISTRATION NUMBER: 39,777
REFERENCE/DOCKET NUMBER: MBL2010 (WO/US)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-362-3800
TELEFAX: 415-362-2928
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

;;
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-635-928-32

Query Match 27.3%; Score 23.5; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

Oy 6 MGKKE-----DLIW 14
||| |:
2 MNGKCVYFCHLDIIV 17

Db

RESULT 11
US-08-635-928-33
; Sequence 33, Application US/08635928
; Patent No. 6291639
; GENERAL INFORMATION:
; APPLICANT: CONRAD, JURGEN
; APPLICANT: DINKELBORG, LUDGER
; APPLICANT: ERBER, SEBASTIAN
; APPLICANT: FROMMEL, CORNELIUS
; APPLICANT: HOHNE, WOLFGANG
; APPLICANT: KRAMPE, WOLFGANG
; APPLICANT: KUTTNER, GABRIELE
; APPLICANT: MALIN, REINHARD
; APPLICANT: SCHIER, HANS MARTIN
; APPLICANT: SCHNEIDER-MERGENER, JENS
; TITLE OF INVENTION: METAL-BINDING CYSTEINE-FREE
; TITLE OF INVENTION: PEPTIDES FOR DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTICAL PURPOSES,
; TITLE OF INVENTION: METHODS FOR THEIR
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEISLER, DUBB, MEYER & LOVEJOY LLP
; STREET: Four Embarcadero Center, Suite 400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635, 928
; FILING DATE: 09/20/96
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: PCT/DE94/01302
; FILING DATE: 10/27/94
; APPLICATION NUMBER: P4337599.5
; FILING DATE: 11/01/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Molano, Michael A.
; REGISTRATION NUMBER: 39, 777
; REFERENCE/DOCKET NUMBER: WBLT2010 (WO/US)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-362-3800
; TELEFAX: 415-362-2928
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal

;; ORIGINAL SOURCE:
US-08-635-928-33

Query Match 27.3%; Score 23.5; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

Oy 6 MGKKE-----DLIW 14
||| |:
2 MNGKCVYFCHLDIIV 17

Db

RESULT 12
US-08-333-565-14
; Sequence 14, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333, 565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-14

Query Match 26.7%; Score 23; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 RSMGKED 11
||| |:
4 RONGMED 11

Db

RESULT 13
US-08-382-013A-9
; Sequence 9, Application US/08382013A
; Patent No. 5631222
; GENERAL INFORMATION:
; APPLICANT: Shidata, Kenji
; APPLICANT: Suzawa, Toshiyuki
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Tanaka, Takeo
; APPLICANT: Tsukuda, Riji
; APPLICANT: Yamada, Koji

APPLICANT: Ohno, Tetsuji
TITLE OF INVENTION: Endothelin-Antagonizing Peptide
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,013A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 155031/93
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lipfert, Nels T.
REGISTRATION NUMBER: 25888
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8200
TELEFAX: 212-354-8113
TELEX: 233188
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-382-013A-9

Query Match 26.7%; Score 23; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIW 14
DB 14 DLIW 17

RESULT 14
US-08-321-625-52
Sequence 52, Application US/08321625
Patent No. 5639860
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. 5639860th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,625
FILING DATE: 12-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-321-625-52

Query Match 26.7%; Score 23; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIW 14
DB 14 DLIW 17

RESULT 15
US-08-661-479-14
Sequence 14, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-14

Query Match 26.7%; Score 23; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 RSMGKED 11
| | | |
Db 4 RONGWED 11

Search completed: June 13, 2006, 01:45:09
Job time : 49 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 01:59:24 ; Search time 66 Seconds
(without alignments)
119.313 Million cell updates/sec

Title: US-10-612-162A-1
Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapex 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 11945

Minimum DB seq length: 17
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	43	50.0	17	5	US-10-801-990-7
3	30	34.9	17	4	US-10-291-241-85
4	28.5	33.1	17	4	US-10-356-257-295
5	28	32.6	17	3	US-09-853-253-14
6	28	32.6	17	3	US-09-798-116-23
7	28	32.6	17	4	US-10-921-371-14
8	27	31.4	17	4	US-10-349-507-15
9	27	31.4	17	4	US-10-267-565-15
10	26	30.2	17	4	US-10-356-257-263
11	26	30.2	17	6	US-11-008-653-145
12	25.5	29.7	17	4	US-10-356-257-243
13	25	29.1	17	3	US-09-845-160-4
14	25	29.1	17	4	US-10-289-454-376
15	25	29.1	17	4	US-10-346-190-157
16	25	29.1	17	4	US-10-428-254A-9
17	25	29.1	17	4	US-10-428-254A-92
18	25	29.1	17	4	US-10-289-456-157
19	25	29.1	17	4	US-10-382-478A-10
20	25	29.1	17	4	US-10-622-124-100
21	25	29.1	17	4	US-10-622-087-70
22	25	29.1	17	6	US-11-037-396-62
23	24	27.9	17	3	US-09-988-493-251
24	24	27.9	17	5	US-10-481-261-225
25	24	27.9	17	5	US-10-834-397-229
26	23.5	27.3	17	4	US-10-356-257-254
27	23.5	27.3	17	4	US-10-356-257-320

28	23	26.7	17	3	US-09-779-323-2	Sequence 2, Appli
29	23	26.7	17	3	US-09-798-116-12	Sequence 12, Appli
30	23	26.7	17	3	US-09-750-754-52	Sequence 52, Appli
31	23	26.7	17	4	US-10-225-567A-2250	Sequence 2250, Ap
32	23	26.7	17	4	US-10-189-437-557	Sequence 557, App
33	23	26.7	17	4	US-10-428-254A-102	Sequence 102, App
34	23	26.7	17	4	US-10-356-257-269	Sequence 269, App
35	23	26.7	17	4	US-10-713-394-2	Sequence 2, Appli
36	23	26.7	17	4	US-10-716-029-196	Sequence 196, App
37	23	26.7	17	4	US-10-806-038-57	Sequence 57, Appli
38	23	26.7	17	5	US-10-481-261-222	Sequence 222, App
39	23	26.7	17	5	US-10-481-261-224	Sequence 224, App
40	23	26.7	17	5	US-10-481-261-226	Sequence 226, App
41	23	26.7	17	5	US-10-783-311-284	Sequence 284, App
42	23	26.7	17	5	US-10-783-311-316	Sequence 316, App
43	23	26.7	17	5	US-10-860-050-570	Sequence 570, App
44	23	26.7	17	5	US-10-945-853-3	Sequence 3, Appli
45	22	25.6	17	3	US-09-864-761-4414	Sequence 4414, A

ALIGNMENTS

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RESULT 1
US-10-612-162-1
; Sequence 1, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; TITLE OF INVENTION: antibodies, their preparation and use
; FILE REFERENCE: 2002/B001
; CURRENT FILING DATE: US/10/612.162
; PRIOR APPLICATION NUMBER: 2003-07-03
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-1

Query Match      100.0%; Score 86; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      1 VVARSMGKEDLIWELL 17

RESULT 2
US-10-801-990-7
; Sequence 7, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schuman, Howard
; TITLE OF INVENTION: Biomarkers for Rheumatoid Arthritis
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801.990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 17
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-7

Query Match
Best Local Similarity 50.0%; Score 43; DB 5; Length 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EDLIEWL 17
Db 1 EDLIEWL 8

RESULT 3
US-10-291-241-85
; Sequence 85, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakodovits
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Mangao Ge
; APPLICANT: Karen Jane Meyrick Morrison
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Pia M. Chailita-Eid
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
; FILE REFERENCE: 51158-20062.20
; CURRENT APPLICATION NUMBER: US/10/291.241
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-291-241-85

Query Match
Best Local Similarity 34.9%; Score 30; DB 4; Length 17;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 GGEEDLIW 14
Db 9 GGEEDLIW 16

RESULT 4
US-10-356-257-295
; Sequence 295, Application US/10356257
; Publication No. US2004008767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FV1a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 295
; LENGTH: 17
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-295

Query Match
Best Local Similarity 33.1%; Score 28.5; DB 4; Length 17;
Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 7 GGEEDLIW 14
Db 3 GGEEDLIW 11

RESULT 5
US-09-853-253-14
; Sequence 14, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:

; APPLICANT: JASPER, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: BISHOP, PAUL
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zs1g33-like peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-14

Query Match
Best Local Similarity 32.6%; Score 28; DB 3; Length 17;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 EDLIEW 15
Db 3 QDLIEW 8

RESULT 6
US-09-798-116-23
; Sequence 23, Application US/09798116
; Patent No. US20020110851A1
; GENERAL INFORMATION:

; APPLICANT: Verhagen, Anne Marie
; APPLICANT: Ekerdt, Paul
; APPLICANT: Vaux, David
; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modulatory Agents Therefor and
; FILE REFERENCE: 10338-004US
; CURRENT APPLICATION NUMBER: US/09/798,116
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: AU PQ5995/00
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: M is methionine sulfoxide
US-09-798-116-23

Query Match
Best Local Similarity 32.6%; Score 28; DB 3; Length 17;

Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KEDLIWEL 17
:|:|:|:
5 EDEWQVI 13

RESULT 7
US-10-921-371-14

; Sequence 14, Application US/10921371
; Publication No. US20050048618A1
; GENERAL INFORMATION:
; APPLICANT: JASPER, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/10/921,371
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-371-14

Query Match 32.6%; Score 28; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EDLWE 15
:|:|:|:
3 QDLWE 8

RESULT 8
US-10-349-507-15

; Sequence 15, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
; APPLICANT: Hekimi, Siegfried
; APPLICANT: Jiang, Ning
; APPLICANT: Benard, Claire
; APPLICANT: Kediir, Hanla
; APPLICANT: McCright, Brenton
; APPLICANT: Lakowski, Bernard
; TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: 11202-006-999
; CURRENT APPLICATION NUMBER: US/10/349,507
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 10/312,187
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/CA01/00913
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/213,174
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/254,932
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-349-507-15

Query Match 31.4%; Score 27; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KEDLIW 14
||| |
1 KEDGIW 6

RESULT 9
US-10-267-565-15

; Sequence 15, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Maurice
; APPLICANT: Gubler, Ulrich
; APPLICANT: Holmes, Jeffery
; APPLICANT: Podlaeki, Frank
; APPLICANT: Stern, Alvin
; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
; TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THERETO
; FILE REFERENCE: 11126-005
; CURRENT APPLICATION NUMBER: US/10/267,565
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 09/401,839
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/459,151
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 08/205,011
; PRIOR FILING DATE: 1994-03-02
; PRIOR APPLICATION NUMBER: 07/857,023
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/572,284
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: 07/520,935
; PRIOR FILING DATE: 1990-05-09
; PRIOR APPLICATION NUMBER: 07/455,708
; PRIOR FILING DATE: 1989-12-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-565-15

Query Match 31.4%; Score 27; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KEDLIW 14
||| |
1 KEDGIW 6

RESULT 10
US-10-356-257-263

; Sequence 263, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: EVI1a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 263
; LENGTH: 17
; TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-356-257-263

Query Match 30.2%; Score 26; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 GKEDLWE 15
Db 3 GVEELWE 10

RESULT 11
US-11-008-653-145
Sequence 145, Application US/11008653
Publication No. US20050175627A1
GENERAL INFORMATION:
APPLICANT: Schneider, Joerg
TITLE OF INVENTION: HIV Pharmacies
FILE REFERENCE: 3742.1001-000
CURRENT APPLICATION NUMBER: US/11/008, 653
CURRENT FILING DATE: 2004-12-09
PRIOR APPLICATION NUMBER: PCT/GB2004/004038
PRIOR FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: GB 0325011.5
PRIOR FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: GB 0322637.0
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB 0322402.9
PRIOR FILING DATE: 2003-09-24
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 145
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide from ref pool 1
US-11-008-653-145

Query Match 30.2%; Score 26; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 KEDLWE 15
Db 8 KEVLVWK 14

RESULT 12
US-10-356-257-243
Sequence 243, Application US/10356257
Publication No. US2004008767A1
GENERAL INFORMATION:
APPLICANT: LAZARUS, ROBERT A.
APPLICANT: MAUN, HENRY R.
TITLE OF INVENTION: Fv1a Antagonists
FILE REFERENCE: P1950R1
CURRENT APPLICATION NUMBER: US/10/356, 257
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/355, 420
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 355
SEQ ID NO 243
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-356-257-243

Query Match 29.7%; Score 25.5; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 4e+03; 1; Indels 1; Gaps 1;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 7 GKEDLW 14
Db 3 GDELEW 11

RESULT 13
US-09-845-160-4
Sequence 4, Application US/09845160
Patent No. US20020058045A1
GENERAL INFORMATION:
APPLICANT: MIZUGUCHI, HIROYUKI
APPLICANT: HAYAKAWA, TAKAO
TITLE OF INVENTION: ADENOVIRUS VECTOR
FILE REFERENCE: 081356/0163
CURRENT APPLICATION NUMBER: US/09/845, 160
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: JP 2001-131688
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: JP 2000-161577
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide having affinity with E-selectin.
US-09-845-160-4

Query Match 29.1%; Score 25; DB 3; Length 17;
Best Local Similarity 42.9%; Pred. No. 4.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLWELL 17
Db 8 DQLWLM 14

RESULT 14
US-10-289-454-376
Sequence 376, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Dennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289, 454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396, 636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050, 902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331, 045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 376
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cepsilon10H3 forward
US-10-289-454-376

Query Match 29.1%; Score 25; DB 4; Length 17;
Best Local Similarity 36.4%; Pred. No. 4.9e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 ARSMGCKEDLI 13
DB 6 SRASGASRDIV 16

RESULT 15

US-10-346-190-157
; Sequence 157, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pellucidol, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-10-346-190-157

Query Match 29.1%; Score 25; DB 4; Length 17;
Best Local Similarity 36.4%; Pred. No. 4.9e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 ARSMGCKEDLI 13
DB 6 SRASGASRDIV 16

Search completed: June 13, 2006, 02:00:46
Job time : 67 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 01:59:49 ; Search time 7 Seconds
(without alignments)
30.705 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 266

Minimum DB seq length: 17
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications AA New:*
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3: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US07_NEW_PUB.pep:*
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8: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	23.3	17	US-10-614-959-22	Sequence 22, Appl
2	20	23.3	17	US-11-251-734-21	Sequence 21, Appl
3	19	22.1	17	US-10-539-402-81	Sequence 81, Appl
4	19	22.1	17	US-11-039-005-5	Sequence 5, Appl
5	17	19.8	17	US-10-539-402-83	Sequence 83, Appl
6	17	19.8	17	US-11-121-282-52	Sequence 52, Appl
7	17	19.8	17	US-11-334-622-12	Sequence 12, Appl
8	16	18.6	17	US-10-508-063A-18	Sequence 18, Appl
9	16	18.6	17	US-10-981-300-62	Sequence 62, Appl
10	16	18.6	17	US-10-981-300-63	Sequence 63, Appl
11	16	18.6	17	US-10-544-050-67	Sequence 67, Appl
12	16	18.6	17	US-11-134-445-68	Sequence 68, Appl
13	16	18.6	17	US-11-122-986-435	Sequence 435, App
14	16	18.6	17	US-11-223-610-172	Sequence 172, App
15	16	18.6	17	US-11-334-622-39	Sequence 39, Appl
16	15	17.4	17	US-10-980-370-20	Sequence 20, Appl
17	15	17.4	17	US-10-984-473-26	Sequence 26, Appl
18	15	17.4	17	US-10-984-473-31	Sequence 31, Appl
19	15	17.4	17	US-10-526-151-27	Sequence 27, Appl
20	15	17.4	17	US-11-176-182-85	Sequence 85, Appl
21	15	17.4	17	US-11-176-182-93	Sequence 93, Appl
22	15	17.4	17	US-11-257-498-59	Sequence 59, Appl
23	15	17.4	17	US-11-298-718-4	Sequence 48, Appl
24	15	17.4	17	US-11-121-282-48	Sequence 30, Appl
25	15	17.4	17	US-11-251-734-30	Sequence 30, Appl

26	15	17.4	17	US-11-132-986-839	Sequence 839, App
27	15	17.4	17	US-11-010-406-10	Sequence 10, Appl
28	14	16.3	17	US-11-300-563-2	Sequence 2, Appl
29	14	16.3	17	US-11-121-282-131	Sequence 131, App
30	14	16.3	17	US-11-251-734-38	Sequence 38, Appl
31	14	16.3	17	US-11-132-986-433	Sequence 433, App
32	14	16.3	17	US-11-142-051-3	Sequence 3, Appl
33	14	16.3	17	US-11-261-429-37	Sequence 37, Appl
34	14	16.3	17	US-11-261-429-39	Sequence 39, Appl
35	13	15.1	17	US-10-706-435A-1	Sequence 1, Appl
36	13	15.1	17	US-10-706-435A-2	Sequence 2, Appl
37	13	15.1	17	US-10-706-435A-7	Sequence 7, Appl
38	13	15.1	17	US-10-706-435A-8	Sequence 8, Appl
39	13	15.1	17	US-10-984-473-43	Sequence 43, Appl
40	13	15.1	17	US-10-984-473-44	Sequence 44, Appl
41	13	15.1	17	US-10-506-063A-39	Sequence 39, Appl
42	13	15.1	17	US-10-519-417-1	Sequence 1, Appl
43	13	15.1	17	US-10-521-401A-22	Sequence 22, Appl
44	13	15.1	17	US-11-176-182-87	Sequence 87, Appl
45	13	15.1	17	US-11-254-195-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-614-959-22
; Sequence 22, Application US/10614959
; Publication No. US20060088534A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Haass, Philipp E.
; APPLICANT: Hass, Philipp E.
; APPLICANT: Justice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/10/614,959
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/383,667
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/098,233
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/122,767
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 22
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-614-959-22
Query Match 23.3%; Score 20; DB 6; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 7 GKKED 11
6 GKKKE 10
RESULT 2
US-11-251-734-21
; Sequence 21, Application US/11251734
; Publication No. US20060100134A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF

```
FILE REFERENCE: HMR2053 US NP1
CURRENT APPLICATION NUMBER: US/11/251.734
CURRENT FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: US 09/933,780
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/222,647
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: GB 0103110.3
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-251-734-21
```

```
Query Match      23.3%; Score 20; DB 7; Length 17;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      8 GKEDLIW 14
      |||
DB      1 GQRIKIW 7
```

```
RESULT 3
US-10-539-402-81
Sequence 81, Application US/10539402
Publication No. US20060115477A1
GENERAL INFORMATION:
APPLICANT: Xerion Pharmaceuticals AG
TITLE OF INVENTION: Tufts University
FILE REFERENCE: XE12EPC
CURRENT APPLICATION NUMBER: US/10/539,402
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 60/435,893
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: EP 03000615
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 17
TYPE: PRT
ORGANISM: human
US-10-539-402-81
```

```
Query Match      22.1%; Score 19; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 DLIV 14
      |
DB      5 DYVW 8
```

```
RESULT 4
US-11-039-005-5
Sequence 5, Application US/11039005
Publication No. US20060115856A1
GENERAL INFORMATION:
APPLICANT: Goldknopf, Ira L.
APPLICANT: Shefa, Essam A.
APPLICANT: Appel, Stanley H.
APPLICANT: Simpson, Ericka P.
APPLICANT: Yen, Albert A.
TITLE OF INVENTION: AN 2'-5'-OLIGODENYLYATE SYNTHETASE LIKE PROTEIN AS A BIOMARKER
FILE REFERENCE: PROT-P0013US
```

```
CURRENT APPLICATION NUMBER: US/11/039,005
CURRENT FILING DATE: 2005-01-19
PRIOR APPLICATION NUMBER: 60/632,218
PRIOR FILING DATE: 2004-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-11-039-005-5
```

```
Query Match      22.1%; Score 19; DB 7; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      8 GKEDL 12
      |||
DB      12 GLEDL 16
```

```
RESULT 5
US-10-539-402-83
Sequence 83, Application US/10539402
Publication No. US20060115477A1
GENERAL INFORMATION:
APPLICANT: Xerion Pharmaceuticals AG
TITLE OF INVENTION: Tufts University
FILE REFERENCE: XE12EPC
CURRENT APPLICATION NUMBER: US/10/539,402
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 60/435,893
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: EP 03000615
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 17
TYPE: PRT
ORGANISM: human
US-10-539-402-83
```

```
Query Match      19.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 GKG 9
      |||
DB      5 GKG 7
```

```
RESULT 6
US-11-121-282-52
Sequence 52, Application US/11121282
Publication No. US20060094862A1
GENERAL INFORMATION:
APPLICANT: Matli Salberg
APPLICANT: Jan-Ingar Flock
TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
FILE REFERENCE: TRIPEP.7AUC4CPIC
CURRENT APPLICATION NUMBER: US/11/121,282
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 10/372,735
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/234,579
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 09/839,666
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 09/532,106
PRIOR FILING DATE: 2000-03-21
```

PRIOR APPLICATION NUMBER: 09/664,945
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/246,258
PRIOR FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 199
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptides
US-11-121-282-52

Query Match 19.8%; Score 17; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KEDLIW 14
Db 2 KESILF 7

RESULT 7
US-11-334-622-12
Sequence 12; Application US/11334622
Publication No. US20060112440A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/11/334,622
CURRENT FILING DATE: 2006-01-17
PRIOR APPLICATION NUMBER: US/09/554,000
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 17
TYPE: PRT
ORGANISM: Gallus gallus
US-11-334-622-12

Query Match 19.8%; Score 17; DB 7; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.7e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 IWE 15
Db 8 MWE 10

RESULT 8
US-10-508-063A-18
Sequence 18; Application US/10508063A
Publication No. US20060088832A1
GENERAL INFORMATION:
APPLICANT: Deutsches Krebsforschungszentrum
APPLICANT: ANGEL, Peter
APPLICANT: FURSTENBERGER, Gerhard
APPLICANT: BREITENBACH, Ute
APPLICANT: RICHTER, Harmut
APPLICANT: HESS, Jochen
APPLICANT: TUCKERMAN, Jan
TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
FILE REFERENCE: 31304-701.831
CURRENT APPLICATION NUMBER: US/10/508,063A
CURRENT FILING DATE: 2004-09-16
NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-508-063A-18

Query Match 18.6%; Score 16; DB 6; Length 17;
Best Local Similarity 37.5%; Pred. No. 5.3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 RSMGKED 11
Db 10 RSKGRRE 17

RESULT 9
US-10-981-300-62
Sequence 62; Application US/10981300
Publication No. US20060093599A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
FILE REFERENCE: ABGX-005
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 62
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-981-300-62

Query Match 18.6%; Score 16; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 5.3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LIW 14
Db 1 VIW 3

RESULT 10
US-10-981-300-63
Sequence 63; Application US/10981300
Publication No. US20060093599A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
FILE REFERENCE: ABGX-005
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-981-300-63

Query Match 18.6%; Score 16; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 5.3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LIW 14
Db 1 VIW 3

```
DB      1 VIM 3

RESULT 11
US-10-544-050-67
; Sequence 67, Application US/10544050
; Publication No. US20060110388A1
; GENERAL INFORMATION:
; APPLICANT: Davies Julian
; TITLE OF INVENTION: Abeta Binding Molecules
; FILE REFERENCE: X-16068
; CURRENT APPLICATION NUMBER: US/10/544,050
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/446380
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: substituted CDR
US-10-544-050-67

Query Match      18.6%; Score 16; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GKE 10
      |||
DB      6 GKE 8

RESULT 12
US-11-134-445-68
; Sequence 68, Application US/11134445
; Publication No. US20060094677A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, CATHERINE
; APPLICANT: CLICHE, DOMINIC
; APPLICANT: HEIKKILA, ELIZABETH MARGARET
; APPLICANT: SENCHYNA, DIANE MICHELLE
; APPLICANT: FLANNAGAN, JOHN GERARD
; APPLICANT: THOMPSON, JOHN E.
; TITLE OF INVENTION: INHIBITION OF APOPTOSIS-SPECIFIC eIF-5A ("eIF-5A1") WITH
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AND siRNAs AS ANTI-INFLAMMATORY
; FILE REFERENCE: 10799/125
; CURRENT APPLICATION NUMBER: US/11/134,445
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 10/792,893
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 10/383,614
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 10/277,969
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 10/200,148
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/141,647
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/909,796
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 60/476,194
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/504,731
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: 60/528,249
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/557,671
; PRIOR FILING DATE: 2004-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95

SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-134-445-68

Query Match      18.6%; Score 16; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GKE 10
      |||
DB      9 GKE 11

RESULT 13
US-11-122-986-435
; Sequence 435, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALFED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 435
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-435

Query Match      18.6%; Score 16; DB 7; Length 17;
Best Local Similarity 41.7%; Pred. No. 5.3e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      6 MGKEDLIWEL 17
      : |||
DB      3 VGSVDLNLLEL 14

RESULT 14
US-11-223-610-172
; Sequence 172, Application US/11223610
; Publication No. US20060111289A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Mizejewski, Gerald J.
; TITLE OF INVENTION: Compositions and Methods of Using Alpha-Fetoprotein Growth
; TITLE OF INVENTION: Inhibitory Peptides
; FILE REFERENCE: HOLLAND-09516
; CURRENT APPLICATION NUMBER: US/11/223,610
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 172
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-223-610-172
```

```
Query Match      18.6%; Score 16; DB 7; Length 17;
Best Local Similarity 60.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ARSMG 7
      || :|
Db      6 ARGVG 10
```

```
RESULT 15
US-11-334-622-39
; Sequence 39, Application US/11334622
; Publication No. US20060112440A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/11/334,622
; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: US/09/554,000
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Calmodulin binding peptide-2
US-11-334-622-39
```

```
Query Match      18.6%; Score 16; DB 7; Length 17;
Best Local Similarity 40.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      13 IWELL 17
      || :|
Db      2 LMKKL 6
```

Search completed: June 13, 2006, 02:00:58
Job time : 7 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 03:50:08 ; Search time 148.824 Seconds
(without alignments)
70.661 Million cell updates/sec

Title: US-10-612-162A-2
Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADAMSIDGCF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_8:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	115	100.0	23	8	ADG46076
2	110	95.7	328	4	AAB84371 Amino CDT
3	110	95.7	539	4	AAU02980 Angiotens
4	110	95.7	575	6	ABR8321 Human met
5	110	95.7	609	8	ABM83782 Human dia
6	110	95.7	627	8	ABM83781 Human dia
7	110	95.7	628	8	ABM83779 Human dia
8	110	95.7	635	8	ADT08174 Human met
9	110	95.7	643	8	ABM83778 Human dia
10	110	95.7	645	4	ABM83783 Human dia
11	110	95.7	646	8	AAU02938 Angiotens
12	110	95.7	646	8	ABM83780 Human dia
13	110	95.7	665	4	AAU02937 Angiotens
14	110	95.7	679	6	ABP72820 Human tra
15	110	95.7	679	8	ADH89360 Human tra
16	110	95.7	679	8	ADK15869 Mature hu
17	110	95.7	679	8	ADL70732 Human tra
18	110	95.7	679	8	ADL24413 Human tra
19	110	95.7	679	8	ADU17885 Human tra
20	110	95.7	679	8	ADT55264 Partial h
21	110	95.7	679	8	ADU07204 Amino aci
22	110	95.7	679	8	ADT78912 Human tra
23	110	95.7	679	8	ADT78149 Human tra

24	110	95.7	679	8	ADT99248 Partial h
25	110	95.7	679	8	ADT35538 Partial h
26	110	95.7	679	8	ADT98423 Human tra
27	110	95.7	679	8	ADU17611 Human tra
28	110	95.7	679	8	ADU17468 Human tra
29	110	95.7	679	8	ADU00630 Human tra
30	110	95.7	679	8	ADT55066 Human par
31	110	95.7	679	9	ADY54149 Amino aci
32	110	95.7	679	9	ADY57102 Human ser
33	110	95.7	679	9	ADY57103 Human ser
34	110	95.7	679	10	AEE47501 Human tra
35	110	95.7	698	2	AAE47501 Human tra
36	110	95.7	698	2	AAE47501 Human tra
37	110	95.7	698	2	AAE47501 Human tra
38	110	95.7	698	2	AAE47501 Human tra
39	110	95.7	698	6	ABP72819 Human ser
40	110	95.7	698	7	ADDA5282 Human pro
41	110	95.7	698	7	ADP74796 Human NOV
42	110	95.7	698	7	ADP74800 Human NOV
43	110	95.7	698	8	ADH34559 Human tra
44	110	95.7	698	8	ADH89359 Human tra
45	110	95.7	698	8	ADK15868 Human tra

ALIGNMENTS

RESULT 1
ADG46076
ID ADG46076 standard; peptide; 23 AA.
XX
AC ADG46076;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDR peptide fragment #2.
XX
DE
XX antibody; carbohydrate-deficient transferrin; CDR;
KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN EP1378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 2; 21pp; German.
XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences VVARSWGCKEDLIWELL, TTEDSIKIMNGEADAMSIDGCF, SKLSMGSLNLESPN and
XX YKRTLEERYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDR
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for

CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilizing it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 115; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
Db 1 TTEDSIKIMNGEADAMSLDGGF 23

RESULT 2
AAB84371
ID AAB84371 standard; protein; 328 AA.
XX
XX AAB84371;
XX
DT 22-AUG-2001 (first entry)
XX
XX Amino acid sequence of a human transferrin.
XX
XX Human; transferrin; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; cerebral ischemia;
XX angiogenesis; nervous system disorder; Alzheimer's disease; infection;
XX ocular disorder; corneal infection; wound healing;
XX epithelial cell proliferation; aging; organ transplant.

XX
XX Homo sapiens.
XX
XX MO200146254-A1.
XX
XX 28-JUN-2001.
XX
XX 21-DEC-2000; 2000MO-US034769.
XX
XX 23-DEC-1999; 99US-0171595P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Shi Y, Choi GH;
XX
XX WPI; 2001-381910/40.
XX
XX N-PSDB; AAS05190.

PT Isolated nucleic acid molecule encoding a human transferrin protein is
PT used in preventing, treating or ameliorating a medical condition.

XX
XX Claim 11; Page 286-287; 290pp; English.

XX
XX The present sequence represents human transferrin polypeptide.
XX Transferrin polypeptides and polynucleotides are used to prevent, treat
XX or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
XX horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
XX treated include autoimmune diseases e.g. rheumatoid arthritis,
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
XX e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi and
XX ocular disorders e.g. corneal infection. The polypeptides can also be
XX used to aid wound healing and epithelial cell proliferation, to prevent
XX skin aging due to sunburn, to maintain organs before transplantation, for
XX supporting cell culture of primary tissues, to regenerate tissues and in
XX chemotaxis. The polypeptides can also be used as a food additive or
XX preservative to increase or decrease storage capabilities

XX
SQ Sequence 328 AA;

Query Match 95.7%; Score 110; DB 4; Length 328;
Best Local Similarity 95.7%; Pred. No. 6.8e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
Db 56 TTEDSIKIMNGEADAMSLDGGF 78

RESULT 3
AAU02980
ID AAU02980 standard; protein; 539 AA.
XX
XX AAU02980;
XX
DT 12-SEP-2001 (first entry)
XX
XX Angiotensin converting enzyme (ACEV) splice variant protein #80.
XX
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
XX platelet-derived endothelial cell growth factor; cardiovascular disease;
XX cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
XX vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
XX myocardial infarction; coronary arterial thrombosis; renal disease;
XX diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
XX multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
XX vascular disorder; asbestosis.

XX
XX Homo sapiens.
XX
XX MO200136632-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000MO-II000766.
XX
XX 17-NOV-1999; 99IL-00132978.
XX
XX 10-DEC-1999; 99IL-00133455.
XX
XX (COMP-) COMPUGEN LTD.
XX
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX
XX WPI; 2001-336004/35.
XX
XX N-PSDB; AAS06080.

PT Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

XX
XX Claim 4; Fig 80; 519pp; English.

XX
XX The sequence represents an angiotensin converting enzyme splice variant
XX (ACEV) polypeptide. The polypeptides of the invention include variants of
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
XX polypeptide receptor 2. The polypeptides and their associated nucleic
XX acids are useful for identification of variant sequences and detection of
XX candidate compounds capable of binding the molecules. The sequences of
XX the invention can be used in the treatment and diagnosis of various
XX disorders including cardiovascular diseases such as arteriosclerosis,
XX myocardial infarction and coronary arterial thrombosis, renal diseases
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX immune disorders such as immune complex nephritis, multiple sclerosis,
XX cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
XX as asbestosis and vascular pathologies involving an endothelial
XX abnormality such as deep vein thrombosis

XX Sequence 539 AA;
SQ
Query Match 95.7%; Score 110; DB 4; Length 539;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTEDSIKINMGADAMSLDGGF 23
DB 265 TTEDCIKINMGADAMSLDGGF 287
RESULT 4
ABR82321
ID ABR82321 standard; protein; 575 AA.
XX
AC ABR82321;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human metalloprotein (MEPR) polypeptide (ID-7509328CD1).
XX
KW MEPR; metalloprotein; anti-HIV; anti-allergic; anti-inflammatory; human;
XX anti-anemic; antiparkinsonian; nootropic; anticonvulsant; cytoprotatic;
XX antidiabetic; antiasthmatic; immunosuppressive; antithyroid;
XX hepatocarcinogenic; dermatological; antidiabetic; nephrotoxic; antilymphoma;
XX thrombotic; neuroprotective; osteoprotective; antirheumatic; uropathic;
XX antiparasitic; antihelminthic; antiparasitic; ophthalmological; virucide;
XX antineoplastic; haemostatic; antibacterial; protozoacide; fungicide;
XX Gene therapy; transgenic.
XX
OS Homo sapiens.
XX
PN WO2003060089-A2.
XX
PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003MO-US001485.
XX
PR 14-JAN-2002; 2002US-0348769P.
XX
PR 18-JAN-2002; 2002US-0350701P.
XX
PR 19-MAR-2002; 2002US-0366059P.
XX
PR 10-MAY-2002; 2002US-0379907P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW;
PI Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Marquis JP;
PI Tang YT;
PI WPI; 2003-598523/56.
DR N-PSDB; ACF35812.
XX
XX New human metalloproteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
PT hepatitis.
XX
XX Claim 1; Page 146-148; 153pp; English.
PS
XX The invention relates to novel human metalloproteins (MEPR) and encoding
CC polynucleotides. The human MEPR polypeptides, polynucleotides and
CC modulators are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MEPR, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,

CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding MEPR are useful for creating transgenic animals
CC to model human disease. Sequences ABR82316-323 represent the human MEPR
CC polypeptides of the invention
XX
SQ Sequence 575 AA;
QY
Query Match 95.7%; Score 110; DB 6; Length 575;
Best Local Similarity 95.7%; Pred. No. 1.3e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTEDSIKINMGADAMSLDGGF 23
DB 269 TTEDCIKINMGADAMSLDGGF 291
RESULT 5
ABR83782
ID ABR83782 standard; protein; 609 AA.
XX
AC ABR83782;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO.4031.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003MO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorn TA, Suchorolski MT, Altus CM, Pits SU, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gershin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
PI Lagace RE, Spito PA, Stewart EH, Wingrove J, Vite UA, Kitron ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACM42434.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC polynucleotide and therapeutic polynucleotides (ditnp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorders, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The ditnp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 609 AA;

SO Query Match 95.7%; Score 110; DB 8; Length 609;
 Best Local Similarity 95.7%; Pred. No. 1.4e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTEDSIKIMNGEADMSLDGCF 23
 DB 321 TTEDCIKIMNGEADMSLDGCF 343

RESULT 6

ABM83781
 ID ABM83781 standard; protein; 627 AA.

AC ABM83781;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

OS WO2004023973-A2.

PN 25-MAR-2004.

PD 12-SEP-2003; 2003WO-US028227.

PF 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Hartshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kitron ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN42433.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

XX Claim 27; Page; 190pp; English.

PS The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorders, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dithp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 627 AA;

SO Query Match 95.7%; Score 110; DB 8; Length 627;
 Best Local Similarity 95.7%; Pred. No. 1.5e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTEDSIKIMNGEADMSLDGCF 23
 DB 321 TTEDCIKIMNGEADMSLDGCF 343

RESULT 7

ABM83779
 ID ABM83779 standard; protein; 628 AA.

AC ABM83779;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4028.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

OS WO2004023973-A2.

PN 25-MAR-2004.

PD 12-SEP-2003; 2003WO-US028227.

PF 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Hartshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kitron ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN42431.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

XX Claim 27; Page; 190pp; English.

PS The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorders, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dithp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dithp protein of the

CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

CC Sequence 628 AA;

Query Match 95.7%; Score 110; DB 8; Length 628;

Best Local Similarity 95.7%; Pred. No. 1.5e-08;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTEDSIKINMGADAMSLDGGF 23

Db 340 TTEDCIKINMGADAMSLDGGF 362

RESULT 8

ADT08174

ID ADT08174 standard; protein: 635 AA.

AC ADT08174;

DT 30-DEC-2004 (first entry)

XX Human metal binding protein (MBP) (ID: 7512697CD1).

XX MBP; metal binding protein; cytosolic; antiarteriosclerotic;
KW anticonvulsant; nootropic; neuroprotective; anti-HIV;
KM anti-allergic; anti-inflammatory; thymomimetic; transgenic; human.

XX Homo sapiens.

XX WO2004085612-A2.

PD 07-OCT-2004.

XX 17-MAR-2004; 2004WO-US008328.

XX 24-MAR-2003; 2003US-0457538P.

XX (INCY-) INCYTE CORP.

PI Jiang X, Jackson AA, Hafalla AJA, Mason PM;

DR WPI; 2004-710307/69.

DR N-PSDB; ADT08177.

PT New human metal binding proteins (MBP), useful for diagnosing, treating
PT and preventing diseases or conditions associated with the aberrant MBP
PT expression e.g. cancer, AIDS, epilepsy, or infections.

PS Claim 1; SEQ ID NO 3; 161pp; English.

XX The invention relates to novel human metal binding proteins (MBP) and
CC encoding polynucleotides. The MBPs can be expressed by standard
CC recombinant methodology. The polypeptides and polynucleotides are useful
CC in diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of MBP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. These are also useful in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of MBP. The MBP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide. An
CC microarray comprising different nucleotide molecules affixed at distinct
CC physical locations on a solid substrate, where at least one nucleotide
CC molecule comprises a first oligonucleotide or polynucleotide sequence
CC specifically hybridizable with at least 30 contiguous nucleotides of the
CC target polynucleotide is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions, and gene expression
CC profiles. The present sequence represents a human MBP.

XX Sequence 635 AA;

Query Match 95.7%; Score 110; DB 8; Length 635;

Best Local Similarity 95.7%; Pred. No. 1.5e-08;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTEDSIKINMGADAMSLDGGF 23

Db 329 TTEDCIKINMGADAMSLDGGF 351

RESULT 9

ABM83778

ID ABM83778 standard; protein: 643 AA.

AC ABM83778;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic pprotein SEQ ID NO:4027.

XX gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.

XX Homo sapiens.

XX WO2004023973-A2.

PD 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Hartschorn TA, Suchorolski MT, Altus CM, Pites SD, Elder LV;

PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LT;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vile UA, Kitron ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.

DR N-PSDB; ACN42430.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, gastrointestinal disorder, endocrine
CC disorder, neurological disorder, gastrointestinal disorder, or
CC infections caused by virus, bacteria, fungi or parasite. The ditnp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence represents a ditnp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 643 AA:

Query Match 95.7%; Score 110; DB 8; Length 643;
Best Local Similarity 95.7%; Pred. No. 1.5e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
|||||
Db 355 TTEDCIKINNGEADAMSLDGCF 377

RESULT 10

ABM83783

ID ABM83783 standard; protein; 645 AA.

AC ABM83783;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pproteins SEQ ID NO:4032.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX Homo sapiens.

XX MO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003MO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmitz JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Harshbome TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV;

XX Mooney EM, Deleage AM, Panzer SR, Bahville SC, Reddy TP;

XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstl EH;

XX Peralta CH, Anderson SB, Rieux P, Shen EJ, Wu MC, Stuve LJ;

XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kiron ES;

XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Patry S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX N-PSDB; ACN42435.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorder, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dthp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germ-line
XX gene therapy. The present sequence represents a dthp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 645 AA:

Query Match 95.7%; Score 110; DB 8; Length 645;

Best Local Similarity 95.7%; Pred. No. 1.5e-08;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
|||||
Db 339 TTEDCIKINNGEADAMSLDGCF 361

RESULT 11

AAU02938

ID AAU02938 standard; protein; 646 AA.

AC AAU02938;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #38.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;

XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;

XX platelet-derived endothelial cell growth factor; cardiovascular disease;

XX cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;

XX vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;

XX myocardial infarction; coronary arterial thrombosis; renal disease;

XX diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;

XX multiple sclerosis; immune complex nephritis; deep vein thrombosis;

XX noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;

XX vascular disorder; asbestosis.

XX Homo sapiens.

XX MO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000MO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00134455.

XX (COMP-) COMPUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstern J;

XX WPI; 2001-336004/35.

XX N-PSDB; AAS06038.

XX Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 3e; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
XX (ACEV) polypeptide. The polypeptides of the invention include variants of
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
XX polypeptide receptor 2. The polypeptides and their associated nucleic
XX acids are useful for identification of variant sequences and detection of
XX candidate compounds capable of binding the molecules. The sequences of
XX the invention can be used in the treatment and diagnosis of various
XX disorders including cardiovascular diseases such as arteriosclerosis,
XX myocardial infarction and coronary arterial thrombosis, renal diseases
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX immune disorders such as immune complex nephritis, multiple sclerosis,
XX cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
XX as asbestosis and vascular pathologies involving an endothelial
XX abnormality such as deep vein thrombosis

SQ Sequence 646 AA:

Query Match 95.7%; Score 110; DB 4; Length 646;
Best Local Similarity 95.7%; Pred. No. 1.5e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTEDSIKINMGADAMSIDGCF 23
Db 392 TTEDCIKINMGADAMSIDGCF 414

RESULT 12
ABM83780
ID ABM83780 standard; protein; 646 AA.
AC ABM83780;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pproetin SEQ ID NO:4029.
DE
XX gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
KW
XX Homo sapiens.
OS
XX MO2004023973-A2.
PN
XX 25-MAR-2004.
PD
XX 12-SEP-2003; 2003WO-US028227.
PF
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmldt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pites ST, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LB;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirron ES;
PI Xu Y, Krong M, Policky JL, Hurwitz BL, Ma Y, Jackson UL, Gierzen D;
PI Pectury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42432.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides
selected from one of the 2722 sequences defined in the specification. A
polynucleotide of the invention may have a use in gene therapy. The human
diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
used to diagnose a particular condition, disease or disorder associated
with human molecules, e.g. cell proliferative disorders,
autoimmune/inflammatory disorder, developmental disorder, endocrine
disorder, neurological disorders, gastrointestinal disorders, or
infections caused by virus, bacteria, fungi or parasite. The ditnp
molecules may also be used in genetic mapping, in identifying individuals
from minute biological samples, in detecting single nucleotide
polymorphisms, as molecular weight markers, and for somatic or germline
gene therapy. The present sequence represents a ditnp protein of the
invention. Note: The sequence data for this patent is not represented in
the printed specification, but was obtained in electronic format directly
from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 646 AA;

Query Match 95.7%; Score 110; DB 8; Length 646;
Best Local Similarity 95.7%; Pred. No. 1.5e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTEDSIKINMGADAMSIDGCF 23
Db 340 TTEDCIKINMGADAMSIDGCF 362

RESULT 13
AAU02937
ID AAU02937 standard; protein; 665 AA.
AC AAU02937;
XX
XX 12-SEP-2001 (first entry)
XX
XX Angiotensin converting enzyme (ACEV) splice variant protein #37.
DE
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW noncardioidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX
XX Homo sapiens.
OS
XX MO200136632-A2.
PN
XX 25-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-IL000766.
PF
XX 17-NOV-1999; 99IL-00132978.
PR 10-DEC-1999; 99IL-00133455.
XX
XX (COMP-) COMPUGEN LTD.
XX
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
PI
PI WPI; 2001-336004/35.
DR N-PSDB; AAS06037.
XX
XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.
PT
XX
XX Claim 4; Fig 37; 519pp; English.

The sequence represents an angiotensin converting enzyme splice variant
(ACEV) polypeptide. The polypeptides of the invention include variants of
granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
platelet-derived endothelial cell growth factor, cyclin-dependent kinase
inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
polypeptide receptor 2. The polypeptides and their associated nucleic
acids are useful for identification of variant sequences and detection of
candidate compounds capable of binding the molecules. The sequences of
the invention can be used in the treatment and diagnosis of various
disorders including cardiovascular diseases such as arteriosclerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases
such as diabetic nephropathy, muscular diseases such as hypertrophy,
immune disorders such as immune complex nephritis, multiple sclerosis,
cancer, sarcoidosis, noncardioidic pulmonary granulomatous diseases such
as asbestosis and vascular pathologies involving an endothelial
abnormality such as deep vein thrombosis

Sequence 665 AA;

FT	Region	581..582	
FT	/note= "Hinge region"		
FT	Binding-site	585	
FT	/note= "Iron binding site"		
FT	Modified-site	611	
FT	/note= "N-glycosylated"		
FT	Region	652..658	
FT	/note= "Hinge region"		
PN	WO2003020746-A1.		
XX			
XX	13-MAR-2003.		
PD			
XX	30-AUG-2002; 2002WO-US027637.		
PF			
XX	30-AUG-2001; 2001US-0315745P.		
PR			
XX	30-NOV-2001; 2001US-0334059P.		
PA	(BIOR-) BIOREXIS PHARM CORP.		
PI	Prior CP;		
XX			
XX	WPI; 2003-332916/31.		
PT			
PT	New fusion protein, useful in the diagnosis and treatment of diseases or disorders relating to the respiratory, cardiovascular and digestive systems, comprises a transferrin protein fused to a therapeutic protein.		
XX			
P5	Disclosure; Page 280-281; 298pp; English.		
XX			
CC	The present sequence is the protein sequence of human transferrin (Tf), minus the signal peptide. The invention relates to modified Tf fusion proteins comprising at least one therapeutic protein, polypeptide or peptide, in which the Tf portion is engineered to extend the serum half-life or bioavailability of the molecule. The modified Tf fusion protein preferably comprises a human Tf moiety that has been modified to reduce or prevent glycosylation, iron binding and/or transferrin receptor binding, having at least one amino acid substitution, deletion or CC addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-188, Lys-206, His-207, His-249, Asp-392, Tyr-426, Tyr-517, His-585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611 (all claimed). Nucleic acids encoding such fusion proteins, vectors, host cells and transgenic animals which produce the fusion protein in their serum or milk are also claimed. The modified fusion protein is useful for treating a disease or disease symptom, or for delivering a therapeutic agent complexed to the ferric iron of transferrin to the inside of a cell or across the blood-brain barrier. The modified fusion protein, or a nucleic acid encoding it, can be used in the diagnosis, prognosis, prevention and/or treatment of diseases and/or disorders of the endocrine, nervous, immune, respiratory, cardiovascular, reproductive and digestive systems, diseases and/or disorders relating to the blood or to cell proliferation, inflammatory conditions, and to treat viral, fungal, bacterial or parasitic infection		
CC			
XX			
XX	Sequence 679 AA;		
QY	Query Match	95.7%; Score 110; DB 6; Length 679;	
	Best Local Similarity	95.7%; Pred. NO. 1.6e-08;	
	Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
DB	1 TTEDSIKINNGEADAMSLDGSF 23		
	373 TTEDCIKINNGEADAMSLDGSF 395		
RESULT 15			
ID	ADH893360		
XX	ADH893360 standard; protein; 679 AA.		
XX	ADH893360;		
DT	15-APR-2004 (first entry)		

XX Human transferrin protein mature amino acid sequence.
 DE fusion protein; transferrin protein; glycosylation;
 XX antibody variable region; cytostatic; antibacterial; virucide;
 KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
 KW viral infection; parasitic infection; neoplasm; autoimmune disease;
 KW arthritis; graft rejection; human.
 XX Homo sapiens.
 OS US2003226155-A1.
 PN 04-DEC-2003.
 PD 10-MAR-2003; 2003US-00384060.
 PF 30-AUG-2001; 2001US-0315745P.
 PR 30-NOV-2001; 2001US-0334059P.
 PR 30-AUG-2002; 2002US-00231494.
 PR 30-AUG-2002; 2002US-0406977P.
 XX (BIOR-) BIOREXIS PHARM CORP.
 PA Sadeghi H, Prior CP, Turner A;
 PI WPI; 2004-022093/02.
 XX N-PDB; ADH89358.
 DR
 XX
 XX New fusion protein comprising a transferrin protein exhibiting reduced
 PT glycosylation fused to at least one antibody variable region, useful for
 PT preparing a composition for treating e.g., septic shock, neoplasm or
 PT autoimmune disease.
 XX
 XX Disclosure; SEQ ID NO 3; 82pp; English.
 PS
 XX This invention relates to a novel fusion protein which comprises a
 CC transferrin protein exhibiting reduced glycosylation fused to at least
 CC one antibody variable region. The invention may be useful for the
 CC development of compounds with cytostatic, antibacterial, virucide,
 CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
 CC the sequences disclosed may be useful for gene therapy. The fusion
 CC protein is useful for preparing a composition for treating a disease or
 CC disease symptom in a patient for example septic shock, endotoxic shock,
 CC cachexia syndromes associated with bacterial, viral or parasitic
 CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
 CC associated with treatment for preventing graft rejection. The present
 CC sequence is that of the mature human transferrin protein which is related
 CC to the invention.
 CC
 SQ Sequence 679 AA;
 QY
 QY 1 TTEDSIKINNGEADAMSLDGF 23
 Db 373 TTEDCIKINNGEADAMSLDGF 395

Search completed: June 13, 2006, 03:58:17
 Job time : 149.824 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:18:14 ; Search time 23.3382 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-2
Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADAMSLOGCF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.80:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	95.7	698	1	TFHUP
2	101	87.8	694	1	TFRBP
3	96	83.5	706	2	S33761
4	92	80.0	311	2	A28446
5	92	80.0	696	1	S01384
6	92	80.0	703	2	A45543
7	90	78.3	695	2	S49163
8	90	78.3	711	1	TFHUL
9	88	76.5	707	1	A28438
10	86	74.8	704	2	I47228
11	84	73.0	708	2	UC2323
12	77	67.0	705	1	TFCHE
13	77	67.0	708	1	TFBOL
14	71	61.7	717	2	S12100
15	66	57.4	690	2	T11749
16	50	43.5	280	1	G70126
17	48	41.7	609	2	E86780
18	47	40.9	466	2	D72733
19	46	40.0	47	2	S13486
20	46	40.0	737	2	AE0819
21	46	40.0	1238	1	A40185
22	46	40.0	1238	1	S17944
23	46	40.0	1238	1	S17946
24	45.5	39.6	483	2	D8752
25	45.5	39.6	483	2	T15180
26	45	39.1	110	2	E83571
27	45	39.1	288	2	F69973
28	45	39.1	491	2	A86824
29	45	39.1	505	1	PSXR44

30	45	39.1	852	2	D72230	conserved hypothe
31	44	38.3	339	2	G69253	hypothetical prote
32	44	38.3	371	2	A69379	conserved hypothe
33	44	38.3	461	2	D84971	phosphotransferase
34	44	38.3	747	2	E91049	probable cytochrom
35	44	38.3	747	2	A85894	probable cytochrom
36	44	38.3	747	2	E85026	hypothetical prote
37	44	38.3	1012	2	T13603	probable N-methyl-
38	43.5	37.8	187	2	D82794	limbikillin Xf0539
39	43.5	37.8	738	1	TFHUM	melanotransferrin
40	43	37.4	246	2	A64326	hypothetical prote
41	43	37.4	298	2	B71317	hypothetical prote
42	43	37.4	320	2	UC7929	ATP-dependent gluc
43	43	37.4	352	2	AC0259	probable membrane
44	43	37.4	358	2	A82206	protein-glutamate
45	43	37.4	376	2	F72514	probable glucokina

ALIGNMENTS

RESULT 1

TFHUP
transferrin precursor [validated] - human
N:Alternate names: siderophilin
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1982 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
C:Accession: A20981; A92417; A94044; A29090; A3739; I51959; I63133; I54011; I68160; A03
R:Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bregt, P.H.; Baldwin
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A>Title: Human transferrin: cDNA characterization and chromosomal localization.
A:Reference number: A20981; MUID:84194084; PMID:6585826
A:Contents: variant C
A:Accession: A20981
A:Molecule type: mRNA
A:Residues: 1-698 <YAN>
A:Cross-references: UNIPROT:P02787, UNIPARC:UPI000002F089; EMBL:M12510; NID:g339452; PID:
A:Note: the authors translated the codon CAA for residue 203 as Glu
R:MacGillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Linbeck-Zins, J.; Brew,
J. Biol. Chem. 258, 3543-3553, 1983
A>Title: The primary structure of human serum transferrin. The structures of seven cyano
A:Reference number: A92417; MUID:83160878; PMID:6833213
A:Accession: A92417
A:Molecule type: protein
A:Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-
A:Cross-references: UNIPARC:UPI0000174483
A:Note: the sequence shown is the predominant electrophoretic genetic variant (C or T/C)
R:Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A>Title: Organization of the human transferrin gene: direct evidence that it originated
A:Reference number: A94044; MUID:85216459; PMID:3858812
A:Accession: A94044
A:Molecule type: DNA
A:Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A:Cross-references: UNIPARC:UPI0000174484; EMBL:M1361
R:Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A>Title: The human transferrin gene: 5' region contains conserved sequences which match
A:Reference number: A29090; MUID:87192006; PMID:3106157
A:Accession: A29090
A:Molecule type: DNA
A:Residues: 1-72; 291-300 <ADR>
A:Cross-references: UNIPARC:UPI000016B0AC; UNIPARC:UPI000016B0AD; EMBL:M15673
R:Uzun, G.; Fraim, M.; Park, I.; Besmond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; Kal
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A>Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A:Reference number: A3739; MUID:84153910; PMID:6322780
A:Accession: A3739
A:Molecule type: mRNA
A:Residues: 422-690, 'G', 692-698 <UZA>
A:Cross-references: UNIPARC:UPI000016B0AB; EMBL:M15525; NID:g339468; PIDN:AAA61142.1; PIR:
R:MacGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Linbeck-Zins, J.; Brew,

Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982
A>Title: The complete amino acid sequence of human serum transferrin.
A/Reference number: A93911; MUID:8222216; PMID:6953407
A/Content: annotation; disulfide bonds
A/Hershberger, C.L.; Larson, J.L.; Arnold, B.; Roseck, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A/Reference number: I51959; MUID:92231399; PMID:1809166
A/Accession: I51959
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-698 <RES>
A/Cross-references: UNIPARC:UPI000016B0AC; GB:S95936; NID:G248647; PIDN:AA61233.1; PID:
R.Duguid, J.R.; Bohm, C.W.; Liu, N.G.; Tourtelotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A/Reference number: I48174; MUID:89386721; PMID:2780570
A/Accession: I63133
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 636-696 <RE2>
A/Cross-references: UNIPARC:UPI000016B13C; GB:M26641; NID:G339988; PIDN:AA61233.1; PID:
R.Schaeffer, E.; Lucero, M.A.; Jeltsch, J.M.; Py, M.C.; Levin, M.J.; Chamoun, P.; Cohen,
Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A/Reference number: I54011; MUID:88056305; PMID:3678832
A/Accession: I54011
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-72 <RE3>
A/Cross-references: UNIPARC:UPI000016B0AC; GB:M17611; NID:G339480; PIDN:AA61147.1; PID:
A/Accession: I68160
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 564-698 <RE4>
A/Cross-references: UNIPARC:UPI000016B0AE; GB:M17614; NID:G339483; PIDN:AA61148.1; PID:
C/Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C/Genes: GDB:TF
A/Cross-references: GDB:I20432; OMIM:190000
A/Map position: 3q21-3q21
A/Intons: 15/1; 72/3; 119/1; 168/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
C/Function:
A/Description: binds iron for delivery into cells
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-698/Product: transferrin #status experimental <MAT>
F/20-350/Domain: transferrin repeat homology <TRH1>
F/356-686/Product: transferrin repeat homology <TRH2>
F/28-67-38-58-137-213-156-350-177-193-180-196-190-198-246-260-358-615-364-396-374-387-42
F/332-630/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 95.7%; Score 110; DB 1; Length 698;
Best Local Similarity 95.7%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
TFRBP
transferrin precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1993 #sequence, revision 30-Sep-1993 #text change 22-Jun-1999
C/Accession: S16246; A61239; G61573; S00335; S02654; A26504; S14853
R/Banfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umehae, T.M.; Woodworth, R.
Biochim. Biophys. Acta 1089, 262-265, 1991
A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
A/Reference number: S16246; MUID:91274362; PMID:2054387
A/Accession: S16246

A/Molecule type: mRNA
A/Residues: 1-694 <BAN>
A/Cross-references: UNIPARC:UPI000016C5CB; EMBL:X58533; NID:G1750; PIDN:CAA41424.1; PID:
R.Pierpaoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
Cell. Immunol. 134, 225-234, 1991
A>Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and endu
A/Reference number: A61239; MUID:9191584; PMID:2013104
A/Accession: A61239
A/Molecule type: protein
A/Residues: 19-36 <PIE>
A/Cross-references: UNIPARC:UPI00001744A6
R/Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
A/Reference number: A61573; MUID:91293379; PMID:2065820
A/Accession: C61573
A/Molecule type: protein
A/Residues: 19-26, 'X', 28-36, 'X', 38-53 <CHU>
A/Cross-references: UNIPARC:UPI00001744A7
R/Goovac-Zimmermann, J.
Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf
A/Reference number: S00335; MUID:88209278; PMID:3365331
A/Accession: S00335
A/Molecule type: protein
A/Residues: 19-45, 'S', 47-48, 'V', 50 <GOD>
A/Cross-references: UNIPARC:UPI00001744A8
R/Byars, R.W.; Altken, A.; Patel, K.J.
FEBS Lett. 238, 39-42, 1988
A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
A/Accession: S02694; MUID:89005676; PMID:3169252
A/Molecule type: protein
A/Residues: 482-515, 'V', 517-544 <EVA>
A/Cross-references: UNIPARC:UPI00001744A9
A/Note: 516-Ile was also found
R/Heaphy, S.; Williams, J.
Biochem. J. 205, 611-617, 1982
A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-t
A/Reference number: A26504; MUID:83074540; PMID:6816218
A/Accession: A26504
A/Molecule type: protein
A/Residues: 19-24, 'N', 26, 'X', 28-29, 'S' <HEA>
A/Cross-references: UNIPARC:UPI00001744AA
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-694/Product: transferrin #status experimental <MAT>
F/19-349/Domain: transferrin repeat homology <TRH1>
F/355-682/Domain: transferrin repeat homology <TRH2>
F/27-66-37-57-136-212-155-349-176-192-179-195-189-197-245-259-357-611-363-395-373-386-42
F/508/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 87.8%; Score 101; DB 1; Length 694;
Best Local Similarity 87.0%; Pred. No. 7.5e-08;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
S33761
transferrin precursor - horse
N/Alternate names: growth-promoting factor
C/Species: Equus caballus (domestic horse)
C/Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text change 09-Jul-2004
C/Accession: S33761; S02145
R/Carpenter, M.A.; Broad, T.E.
Biochim. Biophys. Acta 1173, 230-232, 1993
A>Title: The cDNA sequence of horse transferrin.
A/Reference number: S33761; MUID:93277958; PMID:8504171

A:Accession: S33761
 A:Molecule type: mRNA
 A:Residues: 1-706 <CAR>
 A:Cross-references: UNIPROT:P27425; UNIPARC:UPI0000137370; EMBL:M69020; NID:g164242; PID
 A:Experimental source: liver; developmental stage adult
 R:Yoshinari, K.; Yuasa, K.; Iga, F.; Mimura, A.
 Biochim. Biophys. Acta 1010, 28-34, 1989
 A:Title: A growth-promoting factor for human myeloid leukemia cells from horse serum idc
 A:Reference number: S02145; MUID:89076897; PMID:2909248
 A:Accession: S02145
 A:Molecule type: protein
 A:Residues: 20-35, 'X', 37, 'X', 39-40, 'X', 43-44 <YOS>
 A:Cross-references: UNIPARC:UPI0000177C56
 C:Complex: monomer
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-706/Product: transferrin #status experimental <MAT>
 F:358-694/Domain: transferrin repeat homology <TRH2>
 F:26-64,36-55,134-215,174-190,177-198,187-200,248-262,360-623,366-398,376-389,423-701,44

Query Match 83.5%; Score 96; DB 2; Length 706;
 Best Local Similarity 82.6%; Pred. No. 4.8e-07;
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TTEDSIKINMGADAMSLDGGF 23
 Db 394 TEDCIKIVGEGADAMSLDGGF 416

RESULT 4
 A28446
 A:transferrin - mouse (fragments)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1999 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004
 A:Accession: A28446; A33482; E88438
 R:Chen, L.H.; Bissell, M.J.
 J. Biol. Chem. 262, 17247-17250, 1987
 A:Title: Transferrin mRNA level in the mouse mammary gland is regulated by pregnancy and
 A:Reference number: A28446; MUID:88086992; PMID:3693348
 A:Accession: A28446
 A:Molecule type: mRNA
 A:Residues: 15-80,81-141,217-251,252-301 <CHE>
 A:Cross-references: UNIPROT:Q92111; UNIPARC:UPI00000E773F; UNIPARC:UPI000016D098; UNIPAR
 A:Note: the authors translated the codon ACC for residue 61 as Tyr, TCC for residue 62 a
 R:Idzeta, R.L.; Behringer, R.R.; Theisen, M.; Huguenyik, J.I.; McKnight, G.S.; Brinster
 Mol. Cell. Biol. 9, 5154-5162, 1989
 A:Title: Expression from the transferrin gene promoter in transgenic mice.
 A:Reference number: A33482; MUID:90097932; PMID:2601714
 A:Accession: A33482
 A:Molecule type: DNA
 A:Residues: 1-14,302-311 <ID2>
 A:Cross-references: UNIPARC:UPI0000177C57; UNIPARC:UPI0000177C58; GB:M30819; GB:M30820
 R:Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: B28438
 A:Molecule type: mRNA
 A:Residues: 86-216 <PEN>
 A:Cross-references: UNIPARC:UPI000016CEB1; GB:J03299; GB:J02737; NID:g198847; PIDN:AAA35
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication

Query Match 80.0%; Score 92; DB 2; Length 311;
 Best Local Similarity 81.8%; Pred. No. 8e-07;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TTEDSIKINMGADAMSLDGG 22
 Db 195 TTEDCIKIVGEGADAMTLDDG 216

RESULT 5
 S01384

A:transferrin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 A:Accession: S01384; A60520; A61573
 R:Baldwin, G.S.; Weinstein, J.
 Nucleic Acids Res. 16, 8720, 1988
 A:Title: Nucleotide sequence of porcine liver transferrin.
 A:Reference number: S01384; MUID:88335629; PMID:3419934
 A:Accession: S01384
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-696 <BAL>
 A:Cross-references: UNIPROT:P09571; UNIPARC:UPI00001130C2; EMBL:X12386; NID:g2126; PIDN:
 A:Note: 308-Arg was also found
 R:Baldwin, G.S.; Bacic, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, B
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A:Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine s
 A:Reference number: A60520; MUID:90227903; PMID:2328566
 A:Accession: A60520
 A:Molecule type: protein
 A:Residues: 1-8, 'X', 10-11, 'X', 13-15 <BA2>
 A:Cross-references: UNIPARC:UPI0000174485
 A:Experimental source: gastric mucosa
 A:Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upta
 R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A:Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
 A:Reference number: A61573; MUID:91293379; PMID:2065820
 A:Accession: A61573
 A:Molecule type: protein
 A:Residues: 1-8, 'X', 10-18, 'XE' <CHU>
 A:Cross-references: UNIPARC:UPI0000174486
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron transport; plasma
 F:1-696/Product: transferrin #status predicted <MAT>
 F:1-335/Domain: transferrin repeat homology <TRH1>

Query Match 80.0%; Score 92; DB 1; Length 696;
 Best Local Similarity 81.8%; Pred. No. 2e-06;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TEDSIKINMGADAMSLDGGF 23
 Db 378 TEDCIKIVGEGADAMSLDGGY 399

RESULT 6
 A45543
 A:lactoferrin precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text_change 09-Jul-2004
 A:Accession: A45543; S24173
 R:Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
 Anim. Genet. 23, 251-256, 1992
 A:Title: Cloning and sequencing of the porcine lactoferrin cDNA.
 A:Reference number: A45543; MUID:92367939; PMID:1503259
 A:Accession: A45543
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-703 <ALE>
 A:Cross-references: UNIPROT:P14632; UNIPARC:UPI0000177C55
 A:Experimental source: mammary gland
 A:Note: sequence extracted from NCBI backbone (NCBI:111151, NCBI:P:111153)
 R:Ludon, J.P.; O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Connely, O.M.
 Biochim. Biophys. Acta 1132, 91-99, 1992
 A:Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A:Reference number: S24173; MUID:92379101; PMID:1511016
 A:Accession: S24173
 A:Molecule type: mRNA
 A:Residues: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
 A:Cross-references: UNIPARC:UPI000016CE62; EMBL:M92089; NID:g164613; PIDN:AAA1102.1; PI

A:Experimental source: mammary gland
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-703/Product: lactoferrin #status predicted <MNT>
F:20-350/Domain: transferrin repeat homology <TRH1>
F:36-48/Region: antimicrobial
F:354-691/Domain: transferrin repeat homology <TRH2>
F:28-62,38-53,129-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,49
F:77,107,206,267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
F:135/Binding site: carbonate (Arg) #status predicted
F:409,447,540,609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
F:477/Binding site: carbonate (Arg) #status predicted
F:490/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.0%; Score 92; DB 2; Length 703;
Best Local Similarity 73.9%; Pred. No. 2e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSTAKINGRADMSLDG 23
Db 390 TTEDCIVQVKGADAMSLDG 412

RESULT 7

Transferrin precursor - rat
N:Alternate names: lung-derived growth factor; siderophilin
C:Species: Rattus norvegicus (Norway rat)
C/Date: 16-Feb-1995 #sequence revision 12-May-1995 #text change 09-Jul-2004
C/Accession: S49163; S54980; A30014; A14679; A53289; A30512; I52203
R:Schriver, H.; Pierce, A.; Codeville, B.; Gonzalez, F.; Benaisse, M.; Leger, D.; Wierus
submitted to the EMBL Data Library, January 1994
A:Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
A:Reference number: S49163
A:Accession: S49163
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <ESG>
A:Cross-references: UNIPROT:P12346; UNIPROT:Q63602; UNIPARC:UP10000167A8E; EMBL:X77158;
R:Schriver, H.; Pierce, A.; Codeville, B.; Gonzalez, F.; Benaisse, M.; Leger, D.; Wierus
Biochem. J. 307, 47-55, 1995
A>Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and
A:Reference number: S54980; MUID:95234054; PMID:7717992
A:Accession: S54980
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <ES2>
A:Cross-references: UNIPARC:UP10000167A8E; EMBL:X77158; NID:9510195; PIDN:CAA54403.1; P
R:Hugueny, J.L.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
Endocrinology 120, 332-340, 1987
A>Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulat
A:Reference number: A30014; MUID:87053639; PMID:3023031
A:Accession: A30014
A:Molecule type: mRNA
A:Residues: 518-687, 'D', 689-692, 'TA', 695 <HNG>
A:Cross-references: UNIPARC:UP10000170B4C; GB:M27966; NID:g207439; PIDN:AAA42267.1; PID
R:Schriver, G.; Dryburgh, H.; Miller, A.; Matsuda, Y.; Ingalls, A.; Phillips, J.; Ed
J. Biol. Chem. 254, 12013-12019, 1979
A>Title: The synthesis and secretion of rat transferrin.
A:Reference number: A14679; MUID:80049855; PMID:500689
A:Accession: A14679
A:Molecule type: protein
A:Residues: 20-47 <SCH>
A:Cross-references: UNIPARC:UP10000177C51
R:Cavanaugh, P.G.; Nicolson, G.L.
J. Cell. Biochem. 47, 261-271, 1991
A>Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tun
A:Reference number: A53289; MUID:92165927; PMID:1791188
A:Accession: A53289
A:Status: preliminary
A:Molecule type: protein
A:Residues: 89, 'Y', 'I', 'A', '93-99, 'V', '101-102, 'N', '233, 'AN', '236-243, '401-406, 'N', '408 <CAV>

A:Cross-references: UNIPARC:UP10000086F28; UNIPARC:UP100000876D0; UNIPARC:UP10000087E7F
A:Experimental source: lung
A>Note: sequence modified after extraction from NCBI backbone
A>Note: sequence extracted from NCBI backbone (NCBIP:86115, NCBIP:86116, NCBIP:86114)
R:Purves, L.R.; Purves, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.
Biochim. Biophys. Acta 966, 318-327, 1988
A>Title: Properties of the transferrin associated with rat intestinal mucosa.
A:Reference number: A30512; MUID:88327006; PMID:3046665
A:Accession: A30512
A:Molecule type: protein
A:Residues: 20-30/639-643, 'KD', 646, 'LKACD' <PUR>
A:Cross-references: UNIPARC:UP10000177C52; UNIPARC:UP10000177C53
R:Aldred, A.R.; Howlett, G.J.; Schreiber, G.
Biochem. Biophys. Res. Commun. 122, 960-965, 1984
A>Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bacter
A:Reference number: I52203; MUID:84307580; PMID:6236811
A:Accession: I52203
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 7-25, 'X', '27-56, 'A', '58-64, 267-295 <RES>
A:Cross-references: UNIPARC:UP10000085C48; GB:M26113; NID:g207437; PIDN:AAA42266.1; PID:
C:Genetics:
A:Gene: TF
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication
F:20-348/Domain: transferrin repeat homology <TRH1>

Query Match 78.3%; Score 90; DB 2; Length 695;
Best Local Similarity 81.8%; Pred. No. 4.2e-06;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSTAKINGRADMSLDG 22
Db 388 TTEDCIVQVKGADAMSLDG 409

RESULT 8

Lactotransferrin precursor [validated] - human
N:Alternate names: lactoferrin
C:Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S741
R:Cho, Y.
submitted to the EMBL Data Library, March 1994
A:Reference number: G06820
A:Accession: G01394
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-711 <CHO>
A:Cross-references: UNIPARC:UP1000013737C; EMBL:U07643; NID:g467236; PIDN:AAB60324.1; P
R:Key, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A:Reference number: S11228; MUID:90384839; PMID:2402455
A:Accession: S11228
A:Molecule type: mRNA
A:Residues: 1-146, 'T', '150-422, 'C', '424-711 <REV>
A:Cross-references: UNIPARC:UP1000015C582; EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID
R:Teng, C.T.; Liu, Y.; Yang, N.; Walner, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferr
A:Reference number: A45401; MUID:93125571; PMID:1480183
A:Accession: A45401
A:Molecule type: DNA
A:Residues: 1-15 <TEN>
A:Cross-references: UNIPARC:UP10000004D; GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIP:122202)
R:Powell, M.J.; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A>Title: Nucleotide sequence of human lactoferrin cDNA.
A:Reference number: S10324; MUID:90326549; PMID:2374734

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A:Accession: S10324
A:Molecule type: mRNA
A:Residues: 3-711 <POW>
A:Cross-references: UNIPARC:UPI000016AC28; EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID
R:Stowell, J. 276, 349-355, 1991
Biochem. J. 276, 349-355, 1991
A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A:Reference number: S15853; MUID:91264786; PMID:2049066
A:Accession: S15853
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 20-31 <ST1>
A:Cross-references: UNIPARC:UPI0000174487
A:Accession: S20841
A:Molecule type: protein
A:Residues: 20-28, 'X', 30-31 <ST2>
A:Cross-references: UNIPARC:UPI0000174487
R:Rado, T. A.; Wei, X.; Benz Jr., E. J.
Blood 70, 989-993, 1987
A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A:Reference number: S07160; MUID:88001031; PMID:3477300
A:Accession: S07160
A:Molecule type: mRNA
A:Residues: 436-487, 'A', 489-711 <RAD>
A:Cross-references: UNIPARC:UPI000016ABE2; EMBL:M18642; NID:g186815; PIDN:AAA6665.1; PI
R:Panella, T. J.; Liu, Y.; Huang, A. T.; Teng, C. T.
Cancer Res. 51, 3037-3043, 1991
A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocy
A:Reference number: A61169; MUID:91235214; PMID:1674448
A:Accession: A61169
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 3-701, 'SWKPVN' <PAN>
A:Cross-references: UNIPARC:UPI000014B632
A:Experimental source: normal breast tissue
R:Metz-Boutigue, M. H.; Jollès, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A:Reference number: A31000; MUID:8507667; PMID:6510420
A:Accession: A31000
A:Molecule type: protein
A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
A:Cross-references: UNIPARC:UPI0000174489
A:Note: this is the final paper in a series
R:Houen, G.; Hoegdall, E. V.; Barkholt, V.; Nørskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affini
A:Reference number: S74119; MUID:97054624; PMID:8899921
A:Accession: S74119
A:Molecule type: protein
A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
A:Cross-references: UNIPARC:UPI000017448A
A:Experimental source: neutrophil granulocytes
C:Genetics:
A:Gene: GDB: LTF
A:Cross-references: GDB: 119368; OMIM: 150210
A:Map position: 3q21.3q23
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron binding; milk
F:1-19/Domains: signal sequence #status predicted <SIG>
F:20-711/Product: lactotransferrin #status experimental <MAT>
F:21-356/Domains: transferrin repeat homology <TRH1>
F:360-699/Domains: transferrin repeat homology <TRH2>
F:720-65, 39-56, 135-210, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
F:157, 498/Binding site: carboxydrase (Asn) (covalent) #status experimental
F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

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Query Match 78.3%; Score 90; DB 1; Length 711;
Best Local Similarity 73.9%; Pred. No. 4.3e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
1 TTEDSIKINMGADAMSLDGGF 23
|||||:::|||||||

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Db 396 TTEDCIALVLKGEADAMSLDGGY 418

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RESULT 9
A28438
lactoferrin precursor - mouse
N:Alternate names: lactotransferrin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A28438; A41205
R:Pentecost, B. T.; Teng, C. T.
J. Biol. Chem. 262, 10134-10139, 1987
A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
A:Reference number: A92596; MUID:87280033; PMID:3611056
A:Accession: A28438
A:Molecule type: mRNA
A:Residues: 3-707 <PEN>
A:Cross-references: UNIPARC:UPI00001744A4; EMBL:J03298
R:Liu, Y.; Teng, C. T.
J. Biol. Chem. 265, 21880-21885, 1991
A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A:Reference number: A41205; MUID:92042099; PMID:1939212
A:Accession: A41205
A:Molecule type: DNA
A:Residues: 1-15 <LIV>
A:Cross-references: UNIPARC:UPI00001744A5; GB:W74778
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein
F:1-19/Domains: signal sequence #status predicted <SIG>
F:20-707/Product: lactotransferrin #status predicted <MAT>
F:358-695/Domains: transferrin repeat homology <TRH2>
F:494/Binding site: carboxydrase (Asn) (covalent) #status predicted

```

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Query Match 76.5%; Score 88; DB 1; Length 707;
Best Local Similarity 73.9%; Pred. No. 8.9e-06;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Query Match 73.9%; Score 86; DB 2; Length 704;
Best Local Similarity 78.3%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 TTEDSIKINMGADAMSLDGGF 23
|||||:::|||||||
Db 388 TTEDCIALVLKGEADAMSLDGGF 410

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RESULT 11

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A:Molecule type: mRNA
A:Residues: 1-708 <TSA>
A:Cross-references: UNIPROT:P24627; UNIPARC:UPI0000137377; GB:L08604; NID:9163269; PIDN:
R:Pierce, A.
Submitted to the EMBL Data Library, November 1990
A:Reference number: S14674
A:Accession: S14674
A:Molecule type: mRNA
A:Residues: 1-144, 'V', 146-163, 'P', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <P11>
A:Cross-references: UNIPARC:UPI000016C335; EMBL:X57084; NID:9505; PIDN:CAA40366.1; PID:G
R:Pierce, A.; Colavizza, D.; Benaisa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
Eur. J. Biochem. 196, 177-184, 1991
A>Title: Molecular cloning and sequence analysis of bovine lactoferrin.
A:Reference number: S14110; MUID:91160550; PMID:2001696
A:Accession: S14110
A:Molecule type: mRNA
A:Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <P12>
A:Cross-references: UNIPARC:UPI000017448B; EMBL:X57084
A:Accession: S18517
A:Molecule type: Protein
A:Residues: 20-35, 82-114, 148-163, 'P', 166-178, 'V', 'P', 183-190, 205-212, 230-239, 304-339, 59
A:Cross-references: UNIPARC:UPI000017448C; UNIPARC:UPI000017448D; UNIPARC:UPI000017448E;
493; UNIPARC:UPI0000174494
R:Goodman, R.E.; Schanbacher, F.L.
Biochem. Biophys. Res. Commun. 180, 75-84, 1991
A>Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary gland
A:Reference number: J10595; MUID:92028986; PMID:1718281
A:Accession: J10595
A:Molecule type: mRNA
A:Residues: 1-65, 'P', 68-296, 'S', 298-339, 'A', 341-708 <GCO>
A:Cross-references: UNIPARC:UPI0000174495; GB:M63502
A>Note: The authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
R:Mead, P.E.; Tweedle, J.W.
Nucleic Acids Res. 18, 7167, 1990
A>Title: cDNA and protein sequence of bovine lactoferrin.
A:Reference number: S13097; MUID:91088328; PMID:2263492
A:Accession: S13097
A:Molecule type: mRNA
A:Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
A:Cross-references: UNIPARC:UPI0000174496; EMBL:X54801
A:Accession: S18518
A:Molecule type: Protein
A:Residues: 20-47, 59-66, 132-139, 256-277, 278, 305-332, 343-351, 361-363, 586, 587-589, 598-619
A:Cross-references: UNIPARC:UPI0000174493; UNIPARC:UPI0000174497; UNIPARC:UPI0000174498;
49D; UNIPARC:UPI000017449E
R:Mead, P.E.
Submitted to the EMBL Data Library, October 1990
A:Reference number: S13881
A:Accession: S13881
A:Molecule type: mRNA
A:Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
A:Cross-references: UNIPARC:UPI000017449F; EMBL:X54801
R:Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
Comp. Biochem. Physiol. B 93, 929-934, 1989
A>Title: Purification and characterization of bovine lactoferrin from secretions of the
A:Reference number: P10148; MUID:90031466; PMID:2805645
A:Accession: P10148
A:Molecule type: Protein
A:Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
A:Cross-references: UNIPARC:UPI00001744A0
R:Bellamy, W.; Takase, M.; Yamuchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
Biochim. Biophys. Acta 1121, 130-136, 1992
A>Title: Identification of the bactericidal domain of lactoferrin.
A:Reference number: S21756; MUID:92287941; PMID:1599934
A:Accession: S21756
A:Molecule type: Protein
A:Residues: 36-60 <BEL>
A:Cross-references: UNIPARC:UPI00000475A8
R:Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
J. Dairy Sci. 76, 946-955, 1993
A>Title: Separation and characterization of the C-terminal half molecule of bovine lacto
A:Reference number: A56659; MUID:93253156; PMID:8468645
A:Accession: A56659

A:Molecule type: protein
A:Residues: 20-25, 302-308, 359-366, 'X', 368-376, 'X', 378 <SHT>
A:Cross-references: UNIPARC:UPI00001744A1; UNIPARC:UPI00001744A2; UNIPARC:UPI00001744A3
A:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-708/Product: lactoferrin #status experimental <MAT>
F:20-355/Domain: transferrin repeat homology <TRH1>
F:36-60/Region: antimicrobial
F:359-696/Domain: transferrin repeat homology <TRH2>
F:28-64, 134-217, 176-192, 179-200, 189-202, 250-264, 367-399, 377-390, 424-703, 444-666, 476-551,
F:38-55/Disulfide bonds: #status predicted
F:79, 111, 211, 272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F:140/Binding site: carbonate (Arg) #status experimental
F:252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:414, 452, 545, 614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F:482/Binding site: carbonate (Arg) #status experimental

Query Match 67.0%; Score 77; DB 1; Length 708;
Best Local Similarity 56.5%; Pred. No. 0.0005;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Oy 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 395 TTDDCTIVLKGENDALNDGKY 417

RESULT 14
S12100
transferrin precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text change 09-Jul-2004
C:Accession: S12100
R:Mockaitis, J.E.; Pastor, R.L.; Schoenberg, D.R.
Nucleic Acids Res. 18, 6135, 1990
A>Title: The nucleotide sequence of Xenopus laevis transferrin mRNA.
A:Reference number: S12100; MUID:91045087; PMID:2235503
A:Accession: S12100
A:Molecule type: mRNA
A:Residues: 1-717 <MOS>
A:Cross-references: UNIPROT:P20233; UNIPARC:UPI00001715AD; EMBL:X54530; NID:965158; PIDN
A:Superfamily: transferrin; transferrin repeat homology
F:346-669/Domain: transferrin repeat homology <TRH2>

Query Match 61.7%; Score 71; DB 2; Length 717;
Best Local Similarity 52.2%; Pred. No. 0.0046;
Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 385 TAEEICVQILKGDADAVTLDDGY 407

RESULT 15
T11749
transferrin - Atlantic salmon
C:Species: Salmo salar (Atlantic salmon)
C:Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change 09-Jul-2004
C:Accession: T11749
R:Kingsdal, A.M.; Rorvik, K.A.; Alestrom, P.
Mol. Marine Biol. Biotechnol. 2, 233-238, 1993
A>Title: Cloning and characterization of Atlantic salmon (Salmo salar) serum transferrin
A:Reference number: Z17332; MUID:94122797; PMID:8293074
A:Accession: T11749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-690 <KVI>
A:Cross-references: UNIPROT:P80426; UNIPARC:UPI0000137362; EMBL:L20313; NID:9431609; PID
A:Experimental source: liver
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: iron binding

Query Match 57.4%; Score 66; DB 2; Length 690;

Best Local Similarity 59.1%; Pred. No. 0.028; Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTEDSIAKIMNGEADAMSIDGG 22
| : | | | | : : | |
Db 375 TVEECIKKIMRKEADAIAVDGG 396

Search completed: June 13, 2006, 04:20:35
Job time : 24.3382 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:58:38 ; Search time 185.691 Seconds
(without alignments)
114.574 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSLAKINGEADAMSLDGF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

2849598

Minimum DB seq length: 0

2849598

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	95.7	697	2	Q5R9L7_PONPY
2	110	95.7	698	1	TRFE_HUMAN
3	110	95.7	698	2	Q5R9L7_PONPY
4	110	95.7	698	1	Q5R9L7_PONPY
5	103	89.6	694	2	Q4R5M1_MACFA
6	101	87.8	695	1	Q7TSX8_MARMO
7	96	83.5	706	1	TRFE_HORSE
8	92	80.0	696	1	TRFE_PIG
9	92	80.0	697	2	Q3UBW7_MOUSE
10	92	80.0	697	2	Q3UBW7_MOUSE
11	92	80.0	697	2	Q5R9L7_PONPY
12	92	80.0	704	1	TRFE_BOVIN
13	92	80.0	704	1	TRFL_PIG
14	92	80.0	704	1	Q6Y139_PIG
15	92	80.0	704	2	Q7YS20_PIG
16	92	80.0	704	2	Q8WMN8_PIG
17	90	78.3	698	1	TRFE_RAT
18	90	78.3	698	2	Q7TNK0_RAT
19	90	78.3	710	1	TRFL_HUMAN
20	90	78.3	711	2	Q5DSM0_HUMAN
21	90	78.3	711	2	Q5EKS1_HUMAN
22	90	78.3	979	2	Q7TMC7_RAT
23	90	78.3	980	2	Q7TMC7_RAT
24	88	76.5	705	2	Q6A169_9SAUR
25	88	76.5	707	1	TRFL_MOUSE
26	88	76.5	707	2	Q3TP24_MOUSE
27	88	76.5	707	2	Q3UBV2_MOUSE
28	88	76.5	707	2	Q4FUR3_MOUSE
29	88	76.5	707	2	Q8CBA0_MOUSE
30	87	75.7	700	2	Q8VC96_MOUSE
31	87	75.7	700	2	Q9DBD0_MOUSE

32	87	75.7	709	1	TRFL_CAMDR	Q9TUM0 camelus dro
33	86	74.8	704	2	ICA_PIG	Q29545 sus scrofa
34	84	73.0	421	2	Q7TP83_RAT	Q7TP83 ratius norv
35	84	73.0	708	1	TRFL_BUBBU	Q77698 bubalus bub
36	84	73.0	708	1	TRFL_CAPHI	Q29477 capra hircu
37	83	72.2	695	1	TRFL_HORSE	Q77811 equus caball
38	83	72.2	711	2	Q9XT72_TRIVU	Q9XT72 trichosurus
39	82	71.3	701	2	Q6A168_STRCA	Q6A168 struthio ca
40	80	69.6	462	2	Q6Q147_RAT	Q6Q147 ratius norv
41	80	69.6	708	2	Q5MJE8_SHEEP	Q5MJE8 ovvis aries
42	78	67.8	709	2	Q2TUW9_HUMAN	Q2TUW9 homo sapien
43	77	67.0	355	2	Q8MI10_BOVIN	Q8MI10 bos taurus
44	77	67.0	681	2	Q6LBN7_BOVIN	Q6LBN7 bos taurus
45	77	67.0	705	1	TRFE_CHICK	P02789 gallus gall

ALIGNMENTS

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RESULT 1
Q5R9L7_PONPY PRELIMINARY; PRT; 697 AA.
ID Q5R9L7_PONPY
AC Q5R9L7;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein DKFZP459H0229.
GN Name=DKFZP459H0229;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Oeangger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
CC EMBL: CR859370; CAH91543.1; -; mRNA.
CC
CC SMR: Q5R9L7; 23-346.
CC
CC GO: GO:0005576; C:extracellular region; IEA.
CC GO: GO:0008199; F:ferric iron binding; IEA.
CC GO: GO:0006879; P:iron ion homeostasis; IEA.
CC GO: GO:0006826; P:iron ion transport; IEA.
CC InterPro: IPR011485; Peptidase_S60.
CC PANTHER: PTHR11485; Peptidase_S60.
CC Pfam: PF00405; Transferrin_2.
CC PRINTS: PR00422; TRANSFERRIN.
CC SMART: SM00094; TR_FER_2.
CC PROSITE: PS00205; TRANSFERRIN_1; 2.
CC PROSITE: PS00206; TRANSFERRIN_2; 2.
CC DR PROSITE: PS00207; TRANSFERRIN_3; 2.
CC K1 Hypothetical protein.
CC
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Db 392 TTEDSLAKINGEADAMSLDGF 414
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AC P02787; O43890; G9NQB8; G9UHV0;
DT 21-JUL-1986; integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1989; sequence version 2.
DT 07-MAR-2006; entry version 84.
DE Serotransferrin precursor (Transferrin) (siderophilin) (Beta-1-metal-binding globulin).
GN Name=TF; ORFNames=PRO1400;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS TF*B2; TF*CHI AND TF*D1.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
van Braeg P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal localization."
RT Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,
Chambon P., Cohen G.N., Zakim M.M.;
RT "Complete structure of the human transferrin gene. Comparison with analogous chicken gene and human pseudogene."
RT Gene 56:109-116(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Liver;
MEDLINE=92213399; PubMed=1809186;
RA Herseberger C.L., Larson J.L., Arnold B., Rosteck P.R., Jr.,
Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W., Tice P.A.;
RT "A cloned gene for human transferrin."
RT Ann. N. Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=11110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
Faltjanks V.F.;
RT "Molecular characterization of a case of atransferrinemia."
RT Blood 96:4071-4074(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.;
RT "SeattlesNPc. NHLBI HL66682 program for genomic applications, UM-FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
MEDLINE=22382827; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Tsohynki S., Carninci P., Prange C.T.,
Raha S.S., Loughlin N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Keteeman M., Madan A., Rodriguez S., Sanchez A.,
Fahy J., Helton E., Keteeman M., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
Rauterberg A.C., Krzywicki M.I., Skalek U., Smillius D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Merra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 99-698.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced by analysis of cDNA clones from human fetal liver."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE OF 422-698.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Fraim M., Park I., Besmond C., Maessen G., Trepac J.S.,
Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human transferrin."
RT Biochem. Biophys. Res. Commun. 119:273-281(1984).
RN [9]
RP PROTEIN SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGillivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
Lineback-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of seven cyanogen bromide fragments and the assembly of the complete structure."
RT J. Biol. Chem. 258:3543-3553(1983).
RN [10]
RP NUCLEOTIDE SEQUENCE OF 73-698.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it originated by gene duplication."
RT Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 1-14.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakim M.M.;
RT "The 5' region of the human transferrin gene: structure and potential regulatory sites."
RT Nucleic Acids Res. 14:8692-8692(1986).
RN [12]
RP NUCLEOTIDE SEQUENCE OF 1-72 AND 291-300.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adair G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences that match the control elements regulated by heavy metals,
RT glucocorticoids and acute phase reaction."
RT Gene 49:167-175(1986).
RN [13]
RP NUCLEOTIDE SEQUENCE OF 45-72.
RX MEDLINE=20392111; PubMed=10931525;
DOI=10.1002/1097-4547(200008)51:4<388::AID-JNRS>3.0.CO;2-Q;
RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
Espinoza de los Monteros A., de Veilis J., Zakim M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during differentiation of a human oligodendrocyte cell line."
RT J. Neurosci. Res. 61:388-395(2000).
RN [14]
RP NUCLEOTIDE SEQUENCE OF 564-624, AND VARIANT TF*C2.
RC TISSUE=Brain;
MEDLINE=97418135; PubMed=9272172; DOI=10.1007/s004390050533;
RA Nemerata K., Oyama F., Imagawa M., Ihara Y.;
RT "Human transferrin (TF): a single mutation at codon 570 determines TF C1 or TF C2 variant."
RT Hum. Genet. 100:457-458(1997).
RN [15]
RP NUCLEOTIDE SEQUENCE OF 564-624.
RA Tsuchida S., Ikemoto S., Kajii E.;
RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [16]
RP NUCLEOTIDE SEQUENCE OF 636-696.

RX	MEDLINE=893386721; PubMed=2780570;
RA	Duquid J.R., Bohmont C.W., Liu N.G., Tourtelotte W.W.;
RT	"Changes in brain gene expression shared by scrapie and Alzheimer
RT	disease.";
RL	Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
RN	[17]
RP	PROTEIN SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
RC	TISSUE=Heart;
RX	MEDLINE=96007936; PubMed=7498159;
RA	Kovalyov L.I., Shishkin S.S., Elimochkin A.S., Kovalyova M.A.,
RA	Erbshova E.S., Egorov T.A., Museliamov A.K.;
RT	"The major protein expression profile and two-dimensional protein
RT	database of human heart.";
RL	Electrophoresis 16:1160-1169(1995).
RN	[18]
RP	DISULFIDE BONDS.
RX	MEDLINE=82222166; PubMed=6953407;
RA	McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA	Lienback-Jins J., Brew K.;
RT	"The complete amino acid sequence of human serum transferrin.";
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
RN	[19]
RP	MUTAGENESIS.
RX	MEDLINE=92031536; PubMed=1932003;
RA	Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
RT	"Expression and initial characterization of five site-directed mutants
RT	of the N-terminal half-molecule of human transferrin.";
RL	Biochemistry 30:10824-10829(1991).
RN	[20]
RP	CARBOHYDRATE-LINKAGE SITES ASN-432 AND ASN-630.
RX	PubMed=16335952; DOI=10.1021/pr0502055.
RA	Liu T., Qian W.-Q., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
RA	Moore R.U., Smith R.D.;
RT	"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
RT	hydrazide chemistry, and mass spectrometry.";
RL	J Proteome Res. 4:2070-2080(2005).
RN	[21]
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX	MEDLINE=99272665; PubMed=9609885; DOI=10.1021/bj980355j;
RA	Macgillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
RA	Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang X., Mason A.B.,
RA	Woodworth R.C., Brayer G.D., Baker E.N.;
RT	"Two high-resolution crystal structures of the recombinant N-lobe of
RT	human transferrin reveal a structural change implicated in iron
RT	release.";
RL	Biochemistry 37:7919-7928(1998).
RN	[22]
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX	MEDLINE=99434369; PubMed=9760232; DOI=10.1021/bj9812064;
RA	Jeffrey P.D., Bewley M.C., Macgillivray R.T.A., Macon A.B.,
RA	Woodworth R.C., Baker E.N.;
RT	"Ligand-induced conformational change in transferrins: crystal
RT	structure of the open form of the N-terminal half-molecule of human
RT	transferrin.";
RL	Biochemistry 37:7919-7928(1998).
OY	1 TTEDIATKINGEADMSLDGF 23
DB	392 TTEDIATKINGEADMSLDGF 414
RESULT 3	
OS3H26_HUMAN	
ID	OS3H26_HUMAN PRELIMINARY; PRT; 698 AA.
AC	OS3H26;
DT	24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT	24-MAY-2005, sequence version 1.
DT	07-FEB-2006, entry version 4.
DE	Transferrin variant (Fragment).
OC	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.,
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eucaryotic mRNAs with oligoribonucleotides.";
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=98033986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 RT end-enriched cDNA library.";
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
 RA Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AK227255; BAD96475.1; -, mRNA.
 DR SMR; Q53H26; 23-346.
 DR Ensembl; ENSG00000091513; Homo sapiens.
 DR GO; GO:0005176; C:extracellular region; IEA.
 DR GO; GO:0008199; F:ferrioxalate iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR011156; Peptidase_S60; 1.
 DR Pfam; PF00405; Transferin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SMO0094; TR_PER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 FT NON TER 1
 FT 1
 SQ SEQUENCE 698 AA; 77080 MW; A54775D23B9A4FFFCRC64;

 Query Match 95.7%; Score 110; DB 2; Length 698;
 Best Local Similarity 95.7%; Pred. No. 7,4e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

 Oy 1 TTEDSIKINMGADAMSLDGGF 23
 |||||
 Db 392 TTEDCIKINMGADAMSLDGGF 414

 RESULT 4
 Q4RSML MACFA
 ID Q4RSML_MACFA PRELIMINARY; PRT; 698 AA.
 AC Q4RSML;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Brain cDNA, clone: QCC-13766, similar to human transferrin (TF),
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Cnidaria; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 CC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15944441; DOI=10.1093/molbev/msl187;
 RA Oosada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,

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RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RT Mol. Biol. Evol. 22:1976-1982(2005).
RN
RN
RN
RN
RN NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in drain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative license
CC
CC EMBL: AB169522; BAB01604.1; -, mRNA.
DR SMR; QARSML; 23-346.
DR GO; GO:0005576; Cytoplasmic region; IEA.
DR GO; GO:0008199; Ferritin iron binding; IEA.
DR GO; GO:0006879; Ferritin homeostasis; IEA.
DR GO; GO:0006826; Ferritin transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 698 AA; 77010 MW; F19A15A7C898399B CRC64;

Query Match 95.7%; Score 110; DB 2; Length 698;
Best Local Similarity 95.7%; Pred. No. 7.4e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKINNGEADMSLDGCF 23
Db 392 TTEDCIKINNGEADMSLDGCF 414

RESULT 5
Q7TSX8 MARMO PRELIMINARY; PRT; 694 AA.
ID Q7TSX8 MARMO PRELIMINARY; PRT; 694 AA.
AC Q7TSX8;
DT 01-OCT-2003. Integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003. Sequence version 1.
DT 07-FEB-2006. Entry version 11.
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Sciuridae; Xerinae; Marmotini; Marmota.
OX NCBI_TaxID=9995;
RN
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Rinaldo J.A.S., Gerin J.L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative license
CC
CC EMBL: AY288100; AAP37129.1; -, mRNA.
DR HSSP; P19134; 1UNF.
DR GO; GO:0005576; Cytoplasmic region; IEA.
DR GO; GO:0008199; Ferritin iron binding; IEA.
DR GO; GO:0006879; Ferritin homeostasis; IEA.
DR GO; GO:0006826; Ferritin transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.

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DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 694 AA; 76466 MW; 40053F7DC1FC8A7 CRC64;

Query Match 89.6%; Score 103; DB 2; Length 694;
Best Local Similarity 87.0%; Pred. No. 8.9e-07;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKINNGEADMSLDGCF 23
Db 392 TTEDCIKINNGEADMSLDGCF 414

RESULT 6
TRFE_RABBIT STANDARD; PRT; 695 AA.
ID TRFE_RABBIT STANDARD; PRT; 695 AA.
AC P19134; O46514;
DT 01-NOV-1990. Integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1999. Sequence version 4.
DT 07-MAR-2006. Entry version 61.
DE Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1 metal-
DE binding globulin).
GN Name=TF;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN
RN NUCLEOTIDE SEQUENCE (MRNA).
RC TISSUE=Liver;
RX MEDLINE=91274362; PubMed=2054387; DOI=10.1016/0167-4781(91)90021-D;
RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umlas T.M.,
RA Woodworth R.C., Macgillivray R.T.A.;
RT "The nucleotide sequence of rabbit liver transferrin cDNA.";
RL Biochim. Biophys. Acta 1089:262-265(1991).
RN
RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RC STRAIN=New Zealand white;
RA Gharieb B.A.A., Thepot D., Puisant C., Cajero-Juarez M.,
RA Houdeline L.M.;
RT "Cloning and structural organisation of the rabbit transferrin
RT encoding gene.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN
RN PROTEIN SEQUENCE OF 20-51.
RX MEDLINE=88209278; PubMed=3365331;
RA Godovac-Zimmermann J.;
RT "Isolation, characterization and N-terminal amino-acid sequence of
RT rabbit transferrin.";
RL Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN
RN PROTEIN SEQUENCE OF 483-545.
RX MEDLINE=89005676; PubMed=3169252; DOI=10.1016/0014-5793(88)80221-7;
RA Evans R.W., Aitken A., Patel K.J.;
RT "Evidence for a single glycan moiety in rabbit serum transferrin and
RT location of the glycan within the polypeptide chain.";
RL FEBS Lett. 238:39-42(1988).
RN
RN X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=3179277;
RA Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Haenlein S.,
RA Horburch C., Jhoti H., Lindley P.F., Mydin A., Sarra R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.";
RL Biochemistry 27:5804-5812(1988).
RN
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sarra R., Garratt R.C., Gorinsky B., Jhoti H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin:
RT preliminary structure analysis of the N-terminal half-molecule at 2.3-
RT A resolution.";
RL Acta Crystallogr. B 46:763-771(1990).

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CC -|- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two Fe(3+) ions in association with the binding of an
CC anion, usually bicarbonate. It is responsible for the transport of
CC iron from sites of absorption and heme degradation to those of
CC storage and utilization. Serum transferrin may also have a further
CC role in stimulating cell proliferation.
CC -|- SUBUNIT: Monomer.
CC -|- SUBCELLULAR LOCATION: Secreted protein.
CC -|- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -|- MISCELLANEOUS: The peptidase S60 domains do not have protease
CC function as the catalytic residues are missing.
CC -|- SIMILARITY: Belongs to the transferrin family.
CC -|- SIMILARITY: Contains 2 peptidase S60 domains.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: X56533; CAA41424.1; -, mRNA.
CC
DR EMBL: AF031625; AAB84136.1; -, Genomic DNA.
DR EMBL: AF031611; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031612; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031613; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031614; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031615; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031616; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031617; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031618; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031619; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031620; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031621; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031622; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031623; AAB84136.1; JOINED; Genomic DNA.
DR EMBL: AF031624; AAB84136.1; JOINED; Genomic DNA.
DR PDB: 1JNF; X-ray; A=20--695.
DR PDB: 1TFD; X-ray; @=20-323.
DR MEROPS: S60.972; -.
DR MEROPS: S60.975; -.
DR LinkHub; P19134; -.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Ion transport;
KW Iron; Iron transport; Metal-binding; Methylation; Repeat; Signal;
KW Iron transport.
KW
KW SIGNAL
FT CHAIN 1 19
FT 20 695
FT DOMAIN 25 347
FT DOMAIN 361 680
FT METAL 82 82
FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
FT METAL 411 411
FT METAL 444 444
FT METAL 533 533
FT METAL 601 601
FT BINDING 139 139
FT BINDING 143 143
FT BINDING 145 145
FT BINDING 146 146
FT BINDING 470 470
FT BINDING 474 474
FT BINDING 476 476
FT BINDING 477 477
FT MOD_RSS 42 42
FT CARBOHYD 509 509

FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 612
FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 631 636
FT VARIANT 517 517
FT VARIANT 7 7
FT CONFLICT 47 47
FT CONFLICT 50 50
FT CONFLICT 27 29
FT STRAND 31 31
FT STRAND 32 45
FT HELIX 32 45
FT TURN 46 48
FT STRAND 49 49
FT STRAND 51 53
FT STRAND 59 60
FT STRAND 62 63
FT STRAND 64 72
FT HELIX 73 74
FT TURN 75 75
FT STRAND 78 81
FT STRAND 83 90
FT HELIX 91 94
FT TURN 96 102
FT STRAND 105 105
FT STRAND 107 109
FT STRAND 112 112
FT STRAND 114 121
FT TURN 122 123
FT TURN 128 129
FT TURN 132 133
FT STRAND 136 137
FT STRAND 139 139
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT TURN 155 157
FT STRAND 158 158
FT STRAND 160 160
FT STRAND 163 164
FT HELIX 165 170
FT TURN 171 172
FT STRAND 173 177
FT TURN 179 180
FT STRAND 190 193
FT TURN 194 195
FT STRAND 198 200
FT STRAND 202 206
FT STRAND 207 214
FT HELIX 215 217
FT STRAND 218 225
FT TURN 226 227
FT HELIX 228 232
FT HELIX 236 239
FT TURN 240 241

Query Match 87.8%; Score 101; DB 1; Length 695;
Best Local Similarity 87.0%; Pred. No. 1.8e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      1 TTEDSIKINNGEADMSLDGCF 23
DB      392 STEDCIKINNGEADMSLDGCV 414

RESULT 7
TREE_HORSE
ID      TREE_HORSE      STANDARD;      PRT;      706 AA.
AC      P27425;
DT      01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT      01-AUG-1992, sequence version 1.
DT      21-FEB-2006, entry version 48.
DE      Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1 metal-
DE      binding globulin).
GN      Name=TF;
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX      NCBI_TaxID=9796;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RX      MEDLINE=93277958; PubMed=8504171; DOI=10.1016/0167-4781(93)90186-H;
RA      Carpenter M.A., Broad T.E.;
RT      "The cDNA sequence of horse transferrin.";
RL      Biochim. Biophys. Acta 1173:230-232(1993).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      TISSUE=Embryonic tissue;
RA      McDowell K.J., Adams M.H., Baker C.B.;
RL      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Transferrin are iron binding transport proteins which
CC      can bind two Fe(3+) ions in association with the binding of an
CC      anion, usually bicarbonate. It is responsible for the transport of
CC      iron from sites of absorption and heme degradation to those of
CC      storage and utilization. Serum transferrin may also have a further
CC      role in stimulating cell proliferation.
CC      -1- SUBUNIT: Monomer.
CC      -1- SUBCELLULAR LOCATION: Secreted protein.
CC      -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC      -1- MISCELLANEOUS: The peptidase S60 domains do not have protease
CC      function as the catalytic residues are missing.
CC      -1- SIMILARITY: Belongs to the transferrin family.
CC      -1- SIMILARITY: Contains 2 peptidase S60 domains.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
EMBL: M69020; AAA30958.1; -; mRNA.
EMBL: U21127; AAA63684.1; -; mRNA.
DR      PIR, S33761; S33761.
DR      HSSP, P02787; 1A88.
DR      INTERPRO, IPR001156; Peptidase_S60.
DR      PANTHER, PTHR11485; Peptidase_S60; 1.
DR      Pfam, PF00405; Transferrin; 2.
DR      PRINTS, PR00422; TRANSFERRIN.
DR      SMART, SM00094; TR_FER; 2.
DR      PROSITE, PS00205; TRANSFERRIN_1; 2.
DR      PROSITE, PS00206; TRANSFERRIN_2; 2.
DR      PROSITE, PS00207; TRANSFERRIN_3; 2.
KW      Glycoprotein; Iron transport; Iron; Iron transport; Metal-binding;
KW      Methylation; Repeat; Signal; Transport.
FT      SIGNAL      1..19      By similarity.
FT      CHAIN      20..706      Sero transferrin.
FT      DOMAIN      23..349      /FTID=PRO_0000035714.
FT      METAL      363..691      Peptidase S60 1.
FT      METAL      79..79      Peptidase S60 2.
FT      METAL      111..111      Iron 1 (By similarity).
FT      METAL      209..209      Iron 1 (By similarity).
FT      METAL      270..270      Iron 1 (By similarity).
FT      METAL      413..413      Iron 2 (By similarity).
FT      METAL      449..449      Iron 2 (By similarity).

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FT      METAL      544..544      Iron 2 (By similarity).
FT      METAL      612..612      Iron 2 (By similarity).
FT      BINDING      136..136      Carbonate 1 (By similarity).
FT      BINDING      140..140      Carbonate 1 (By similarity).
FT      BINDING      142..142      Carbonate 1; via amide nitrogen (By
FT      BINDING      143..143      similarity).
FT      BINDING      143..143      Carbonate 1; via amide nitrogen (By
FT      BINDING      476..476      similarity).
FT      BINDING      480..480      Carbonate 2 (By similarity).
FT      BINDING      482..482      Carbonate 2; via amide nitrogen (By
FT      BINDING      483..483      similarity).
FT      MOD_RES      40..40      Omega-N-methylated arginine (By
FT      CARBOHYD      515..515      N-linked (GlcNAc...) (Potential).
FT      DISULFID      26..64      By similarity.
FT      DISULFID      36..55      By similarity.
FT      DISULFID      134..215      By similarity.
FT      DISULFID      174..190      By similarity.
FT      DISULFID      177..198      By similarity.
FT      DISULFID      187..200      By similarity.
FT      DISULFID      248..262      By similarity.
FT      DISULFID      360..623      By similarity.
FT      DISULFID      366..398      By similarity.
FT      DISULFID      376..389      By similarity.
FT      DISULFID      423..701      By similarity.
FT      DISULFID      441..664      By similarity.
FT      DISULFID      474..550      By similarity.
FT      DISULFID      498..692      By similarity.
FT      DISULFID      508..522      By similarity.
FT      DISULFID      519..533      By similarity.
FT      DISULFID      590..604      By similarity.
FT      DISULFID      642..647      By similarity.
SQ      SEQUENCE      706 AA; 78095 MW; 1A0FA566C0409D8A CRC64;

Query Match      83.5%; Score 96; DB 1; Length 706;
Best Local Similarity      82.6%; Pred. No. 1,1e-05;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTEDSIKINNGEADMSLDGCF 23
DB      394 STEDCIKINNGEADMSLDGCV 416

RESULT 8
TREE_PIG
ID      TREE_PIG      STANDARD;      PRT;      696 AA.
AC      P09571;
DT      01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
DT      01-FEB-1991, sequence version 2.
DT      21-FEB-2006, entry version 59.
DE      Sero transferrin (Transferrin) (Siderophilin) (Beta-1 metal-binding
DE      globulin).
GN      Name=TF;
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
OC      Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      TISSUE=Liver;
RX      MEDLINE=88335629; PubMed=3419934;
RA      Baldwin G.S., Weinstock J.;
RT      "Nucleotide sequence of porcine liver transferrin.";
RL      Nucleic Acids Res. 16:8720-8720(1988).
RN      [2]
RP      PROTEIN SEQUENCE OF 1-20.
RX      MEDLINE=91293379; PubMed=2065820;
RA      Chung M.C., Chan S.L., Shimizu S.;
RT      "Purification of transferrin and lactoferrin using DEAB affi-gel

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FT HELIX 224 226
FT STRAND 227 230
FT TURN 232 233
FT STRAND 234 234
FT STRAND 236 238
FT HELIX 239 244
FT STRAND 245 245
FT STRAND 247 251
FT STRAND 254 261
FT HELIX 264 278
FT STRAND 279 279
FT TURN 280 281
FT STRAND 282 282
FT STRAND 284 285
FT TURN 288 289
FT TURN 292 293
FT STRAND 295 299
FT TURN 301 302
FT STRAND 305 308
FT TURN 311 312
FT HELIX 315 319
FT HELIX 321 331
FT STRAND 344 344
FT STRAND 346 351
FT HELIX 352 365
FT TURN 366 368
FT STRAND 369 377
FT HELIX 378 386
FT TURN 387 388

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Query Match      80.0%; Score 92; DB 1; Length 696;
Best Local Similarity 81.8%; Pred. No. 4,5e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 2 TEDSIKINMGADAMSLDGGF 23
Db 378 TEDCIATKVGADAMSLDGGY 399

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RESULT 9
TREE MOUSE STANDARD; PRT; 697 AA.
AC 092111; O35421; Q61803; Q62358; Q62359; Q63915; Q64515; Q8V115;
AC 092200;
DT 06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DE 01-MAR-2006, entry version 44.
DE Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal-binding globulin).
GN Name=Tf; Synonyms=Tf;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI Taxid=10090;
RN [1]_Taxid=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Lai D.-2.;
RT "Construction of a robust CHO cell-line for biopharmaceutical production."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX PubMed=16141072; DOI=10.1126/science.1112014;
CA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldins V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

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RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schut N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F., Diatchenko L., Marzula K., Farmer A.A., Rubin G.W., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Umed T.B., Yoshiyuki S., Carninci P., Muliyil S.J., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Muliyil S.J., Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hult S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
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RP NUCLEOTIDE SEQUENCE OF 1-11.
RC STRAIN=BALB/c;
RX MEDLINE=98284323; PubMed=9621303;
RX DOI=10.1002/(SICI)1098-2795(199807)50:3<273::AID-MRD3>3.3.CO;2-C;
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RL Mol. Reprod. Dev. 50:273-283(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 277-337; 462-496 AND 526-575.
RX MEDLINE=88086992; PubMed=4693348;
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 RA "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
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 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RC MEDLINE=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
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 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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 RA Birney E., Hayashizaki Y.;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
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 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RC MEDLINE=1065660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
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 RL Nature 409:685-690(2001).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
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 RT "Riken integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Kanagawa S.,
 RA Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
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 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanuki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AK150782; BAE29847.1; -; mRNA.
 DR MGI: MGI:98821; Trf.
 DR GO: GO:0030139; C:cytosolic vesicle; IDA.
 DR GO: GO:0005768; C:cytosol; IDA.
 DR GO: GO:0005615; C:extracellular space; RCA.
 DR GO: GO:0008199; F:feric iron binding; RCA.
 DR GO: GO:0006879; P:iron ion homeostasis; RCA.
 DR GO: GO:0006826; P:iron ion transport; RCA.
 DR InterPro: IP001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin_2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER_2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 SQ SEQUENCE 697 AA; 76698 MW; D3E37B96B856B525 CRC64;
 Query Match 80.0%; Score 92; DB 2; Length 697;
 Best Local Similarity 81.8%; Pred. NO. 4.5e-05;
 Matches 18; Conservative 2; Mismatches 0; Gaps 0;

QY 1 TTSPSIKINGEADANSLDGG 22
 DB 391 TTEDICIEKIVNGEADAMTLDDG 412

RESULT 11
 Q58B69_MOUSE PRELIMINARY; PRT; 697 AA.
 AC Q58B69;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE Transferrin (10 days lactation, adult female mammary gland cDNA, RIKEN
 full-length enriched library, clone:D730004119 product:transferrin,
 full insert sequence) (17 days pregnant adult female amnion cDNA,
 RIKEN full-length enriched library, clone:1920024003
 product:transferrin, full insert sequence) (Adult male liver tumor
 cDNA, RIKEN full-length enriched library, clone:C730037117
 product:transferrin, full insert sequence) (Adult male liver tumor
 cDNA, RIKEN full-length enriched library, clone:C730048P21
 product:transferrin, full insert sequence) (17 days pregnant adult
 female amnion cDNA, RIKEN full-length enriched library,
 clone:1920015B11 product:transferrin, full insert sequence) (17 days
 pregnant adult female amnion cDNA, RIKEN full-length enriched library,
 clone:1920066F17 product:transferrin, full insert sequence).
 GN Name=Trf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 ON NCBI TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FWB/N. TISSUE=Mammary tumor. C3;
 RX MEDLINE=22398257; PubMed=12479932; DOI=10.1073/pnas.2426039899;
 RA Krausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 Altschuler R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
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 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FWB/N. TISSUE=Mammary tumor. C3;
 RG NIH MGC Project.
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J. TISSUE=Amnion, Liver, and Mammary gland;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J. TISSUE=Amnion, Liver, and Mammary gland;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
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 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J. TISSUE=Amnion, Liver, and Mammary gland;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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 RA Nishikido I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
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CC	can bind two Fe(3+) ions in association with the binding of an
CC	anion, usually bicarbonate.
CC	- FUNCTION: The lactoferrin peptidase S60 domain 1 functions as
CC	a serine protease that cuts arginine rich regions. This function
CC	contributes to the antimicrobial activity (By similarity).
CC	- CATALYTIC ACTIVITY: Preferential at -Arg-Ser-Arg - and -Arg-
CC	Arg-Ser-Arg - , and of Z-Phe-Arg -aminoethylcoumarin.
CC	- SUBUNIT: Monomer.
CC	- I- SUBCELLULAR LOCATION: Secreted protein.
CC	- MISCELLANEOUS: The second peptidase S60 domain does not have
CC	protease function as the catalytic residues are missing.
CC	- SIMILARITY: Belongs to the transferrin family.
CC	- SIMILARITY: Contains 2 peptidase S60 domains.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; M92089; AAA31102.1; -; mRNA.
DR	EMBL; M81327; AAA31059.1; -; mRNA.
DR	HSSP; Q9TUM0; 1DTZ.
DR	InterPro; IPR001156; Peptidase_S60.
DR	Pfam; PF00405; Transferrin_2.
DR	PRINTS; PR00422; TRANSFERRIN.
DR	SMART; SMO0094; TR_PER; 2.
DR	PROSITE; PS00205; TRANSFERRIN_1; 2.
DR	PROSITE; PS00206; TRANSFERRIN_2; 1.
DR	PROSITE; PS00207; TRANSFERRIN_3; 1.
KM	Direct protein sequencing; Glycoprotein; Hydrolase; Ion transport;
KW	Iron; Iron transport; Metal-binding; Protease; Repeat;
KW	Serine protease; Signal; Transport.
FT	CHAIN
FT	1 19
FT	20 704
FT	/Frtid-PRO_0000035738.
FT	DOMAIN
FT	25 348
FT	Peptidase_S60_1.
FT	360 689
FT	Catalytic dyad (By similarity).
FT	ACT_SITE
FT	274 274
FT	METAL
FT	77 77
FT	Iron 1 (By similarity).
FT	METAL
FT	107 107
FT	Iron 1 (By similarity).
FT	METAL
FT	207 207
FT	Iron 1 (By similarity).
FT	METAL
FT	268 268
FT	Iron 1 (By similarity).
FT	METAL
FT	410 410
FT	Iron 2 (By similarity).
FT	METAL
FT	448 448
FT	Iron 2 (By similarity).
FT	METAL
FT	541 541
FT	Iron 2 (By similarity).
FT	METAL
FT	610 610
FT	Iron 2 (By similarity).
FT	BINDING
FT	132 132
FT	Carbonate 1 (By similarity).
FT	BINDING
FT	136 136
FT	Carbonate 1 (By similarity).
FT	BINDING
FT	138 138
FT	Carbonate 1; via amide nitrogen (By similarity).
FT	BINDING
FT	139 139
FT	Carbonate 1; via amide nitrogen (By similarity).
FT	BINDING
FT	474 474
FT	Carbonate 2 (By similarity).
FT	BINDING
FT	478 478
FT	Carbonate 2 (By similarity).
FT	BINDING
FT	480 480
FT	Carbonate 2; via amide nitrogen (By similarity).
FT	BINDING
FT	481 481
FT	Carbonate 2; via amide nitrogen (By similarity).
FT	CARBONYD
FT	385 385
FT	N-linked (GlcNAc . .) (Potential).
FT	CARBONYD
FT	491 491
FT	N-linked (GlcNAc . .) (Potential).
FT	DISULFID
FT	38 62
FT	By similarity.
FT	DISULFID
FT	53 53
FT	By similarity.
FT	DISULFID
FT	130 213
FT	By similarity.
FT	DISULFID
FT	172 188
FT	By similarity.
FT	DISULFID
FT	185 196
FT	By similarity.
FT	DISULFID
FT	246 260
FT	By similarity.
FT	DISULFID
FT	363 395
FT	By similarity.
FT	DISULFID
FT	373 386
FT	By similarity.
FT	DISULFID
FT	420 699
FT	By similarity.
FT	DISULFID
FT	472 547
FT	By similarity.
FT	DISULFID
FT	496 690
FT	By similarity.
FT	DISULFID
FT	506 520
FT	By similarity.

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FT DISULFID 517 530 By similarity.
FT DISULFID 588 602 By similarity.
FT DISULFID 640 643 By similarity.
FT CONFLICT 12 12 G -> W (in Ref. 1).
FT CONFLICT 46 48 RRT -> TTR (in Ref. 3).
FT CONFLICT 51 51 M -> I (in Ref. 1).
FT CONFLICT 85 85 D -> G (in Ref. 2).
FT CONFLICT 121 121 Missing (in Ref. 2).
FT CONFLICT 132 132 T -> I (in Ref. 1).
FT CONFLICT 284 284 E -> S (in Ref. 1).
FT CONFLICT 573 573 E -> Q (in Ref. 1).
FT CONFLICT 590 590 D -> N (in Ref. 1).
FT CONFLICT 625 625 V -> M (in Ref. 1).
FT CONFLICT 662 662 V -> C (in Ref. 1).
FT CONFLICT 686 704 NUKQCSVSPLEKACAFMR -> T (in Ref. 1).
SQ SEQUENCE 704 AA; 77626 MW; 93261EFD608AD358 CRC64;

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Query Match 80.0%; Score 92; DB 1; Length 704;
Best Local Similarity 73.9%; Pred. No. 4.5e-05;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TTEDSIKINNGEADAMSIDGDF 23
DB 391 TTEDCIVQVKGADAMSIDGDF 413

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RESULT 14
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AC Q6Y739;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Lactoferrin.
GN Name=LTF;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
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CC EMBL; AP006185; BAD08651.1; -; Genomic DNA.
CC HSSP; Q29477; 1JW1.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
SQ SEQUENCE 704 AA; 77612 MW; 10DFEA3C1366D5DA CRC64;

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Query Match 80.0%; Score 92; DB 2; Length 704;
Best Local Similarity 73.9%; Pred. No. 4.5e-05;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TTEDSIKINNGEADAMSIDGDF 23
DB 391 TTEDCIVQVKGADAMSIDGDF 413

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RESULT 15
Q7YS20_PIG PRELIMINARY; PRT; 704 AA.
ID Q7YS20;
AC Q7YS20;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Lactoferrin.
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Pecorini C., Fogher C., Baldi A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
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CC EMBL; AY306198; AAP70487.1; -; mRNA.
CC HSSP; P24627; INKX.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
SQ SEQUENCE 704 AA; 77523 MW; AAC8E1767E56BF6A CRC64;

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Query Match 80.0%; Score 92; DB 2; Length 704;
Best Local Similarity 73.9%; Pred. No. 4.5e-05;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TTEDSIKINNGEADAMSIDGDF 23
DB 391 TTEDCIVQVKGADAMSIDGDF 413

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Search completed: June 13, 2006, 04:17:50
Job time : 186.691 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:20:54 ; Search time 40.5882 Seconds
(without alignments)
49.601 Million cell updates/sec

Title: US-10-612-162A-2
Perfect score: 115
Sequence: 1 TTEDSTAKINMGENDAMSLDGGF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCMS.COMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	95.7	698	1	US-08-175-158A-2
2	110	95.7	698	2	US-09-438-740-2
3	110	95.7	1074	1	US-08-470-058-2
4	110	95.7	1074	2	US-09-037-188-2
5	110	95.7	1074	2	US-09-285-310-2
6	110	95.7	1074	2	US-09-753-385-2
7	110	95.7	1410	1	US-08-470-058-4
8	110	95.7	1410	2	US-09-037-188-4
9	110	95.7	1410	2	US-09-285-310-4
10	110	95.7	1410	2	US-09-753-385-4
11	93.5	81.3	696	7	5262177-4
12	92	80.0	697	2	US-09-724-864-54
13	92	80.0	703	1	US-08-145-681-6
14	92	80.0	703	1	US-08-453-703-6
15	92	80.0	703	1	US-08-456-106-6
16	92	80.0	703	2	US-08-456-108-6
17	92	80.0	703	2	US-09-265-577-6
18	92	80.0	703	2	US-09-633-739-6
19	90	78.3	690	2	US-10-077-381-4
20	90	78.3	694	2	US-08-724-586-2
21	90	78.3	694	2	US-09-421-632-2
22	90	78.3	694	2	US-09-932-190-2
23	90	78.3	705	1	US-08-655-640-2
24	90	78.3	708	1	US-08-655-640-4
25	90	78.3	709	1	US-08-154-019-2
26	90	78.3	709	1	US-08-461-333-2

27	90	78.3	709	2	US-08-464-167-2	Sequence 2, Appli
28	90	78.3	709	2	US-09-158-313-2	Sequence 2, Appli
29	90	78.3	709	2	US-08-476-798-2	Sequence 2, Appli
30	90	78.3	711	1	US-08-145-681-2	Sequence 2, Appli
31	90	78.3	711	1	US-08-250-308-2	Sequence 2, Appli
32	90	78.3	711	1	US-08-154-019-4	Sequence 2, Appli
33	90	78.3	711	1	US-08-461-333-4	Sequence 4, Appli
34	90	78.3	711	1	US-08-453-703-2	Sequence 2, Appli
35	90	78.3	711	1	US-08-456-106-2	Sequence 2, Appli
36	90	78.3	711	2	US-08-464-167-4	Sequence 4, Appli
37	90	78.3	711	2	US-09-158-313-4	Sequence 4, Appli
38	90	78.3	711	2	US-08-456-108-2	Sequence 2, Appli
39	90	78.3	711	2	US-08-476-798-4	Sequence 4, Appli
40	90	78.3	711	2	US-09-265-577-2	Sequence 2, Appli
41	90	78.3	711	2	US-09-633-739-2	Sequence 2, Appli
42	90	78.3	711	5	PCT-US93-03614-2	Sequence 2, Appli
43	77	67.0	21	2	US-10-394-980-20	Sequence 20, Appli
44	77	67.0	708	1	US-08-145-681-4	Sequence 4, Appli
45	77	67.0	708	1	US-08-453-703-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-175-158A-2
; Sequence 2, Application US/08175158A
; Patent No. 5986067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MACGILLIVRAY, Ross T. A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOOWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,158A
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,029
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-175-158A-2
Query Match 95.7%; Score 110; Length 698;
Best Local Similarity 95.7%; Pred. No. 1.2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKINNGEADMSLDGCF 23
Db 392 TTEDCIKINNGEADMSLDGCF 414

RESULT 2

US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MASON, Anne B.
APPLICANT: MACGILLIVRAY, Ross T.A.
APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match 95.7%; Score 110; DB 2; Length 698;
Best Local Similarity 95.7%; Pred. No. 1.2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKINNGEADMSLDGCF 23
Db 392 TTEDCIKINNGEADMSLDGCF 414

RESULT 3
US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 95.7%; Score 110; DB 1; Length 1074;
Best Local Similarity 95.7%; Pred. No. 2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKINNGEADMSLDGCF 23
Db 768 TTEDCIKINNGEADMSLDGCF 790

RESULT 4
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janie K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query March 95.7%; Score 110; DB 2; Length 1074;
Best Local Similarity 95.7%; Pred. No. 2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGGF 23
Db 768 TTEDCIKINMGADAMSLDGGF 790

RESULT 5
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query March 95.7%; Score 110; DB 2; Length 1074;
Best Local Similarity 95.7%; Pred. No. 2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTEDSIKINMGADAMSLDGGF 23
Db 768 TTEDCIKINMGADAMSLDGGF 790

RESULT 6
US-09-753-385-2
Sequence 2, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
TITLE OF INVENTION: OF A SELECTED SUBSTANCE INTO CELLS
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1074
TYPE: PRT
ORGANISM: Homo sapiens
US-09-753-385-2

Query March 95.7%; Score 110; DB 2; Length 1074;
Best Local Similarity 95.7%; Pred. No. 2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGGF 23
Db 768 TTEDCIKINMGADAMSLDGGF 790

RESULT 7
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 95.7%; Score 110; DB 1; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 1104 TTEDCIKINNGEADAMSLDGCF 1126

RESULT 8
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
City: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 95.7%; Score 110; DB 2; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 1104 TTEDCIKINNGEADAMSLDGCF 1126

RESULT 9
US-09-285-310-4
Sequence 4, Application US/09285310

Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
City: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 95.7%; Score 110; DB 2; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 1104 TTEDCIKINNGEADAMSLDGCF 1126

RESULT 10
US-09-753-385-4
Sequence 4, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
TITLE OF INVENTION: OF A SELECTED SUBSTANCE INTO CELLS
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4

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; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-753-385-4

Query Match          95.7%; Score 110; DB 2; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGGF 23
Db 1104 TTEDCIKINMGADAMSLDGGF 1126

RESULT 11
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. OSEPH P.; ESTLIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELLSSTROM, KARL E.; ROSE, TIMOTHY M.; HELLSSTROM, INGEGGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 4:
; LENGTH: 696
5262177-4

Query Match          81.3%; Score 93.5; DB 7; Length 696;
Best Local Similarity 91.3%; Pred. No. 6.3e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TTEDSIKINMGADAMSLDGGF 23
Db 392 TTEDCIKINMGADAMSLDGGF 413

RESULT 12
US-09-724-864-54
; Sequence 54, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Marison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-54

Query Match          80.0%; Score 92; DB 2; Length 697;
Best Local Similarity 81.8%; Pred. No. 1.1e-06;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGG 22
Db 391 TTEDCIKINMGADAMSLDGG 412
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RESULT 13
US-08-145-681-6
; Sequence 6, Application US/08145681
; Patent No. 5571691
; GENERAL INFORMATION:
; APPLICANT: Conneely, Orla M.
; APPLICANT: Heaton, Denis R.
; APPLICANT: O'Malley, Bert W.
; APPLICANT: May, Gregory S.
; TITLE OF INVENTION: Production of Recombinant Lactoferrin
; TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
; TITLE OF INVENTION: Various Organisms
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Baker & Bots, L.L.P.
; STREET: 910 Louisiana St
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,681
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcgregor, Martin L.
; REGISTRATION NUMBER: 29,329
; REFERENCE/DOCKET NUMBER: 19928-0125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/229/1874
; TELEFAX: 713/229/1522
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 703 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Sus scrofa
US-08-145-681-6

Query Match          80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 1.1e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGGF 23
Db 390 TTEDCIKINMGADAMSLDGGF 412

RESULT 14
US-08-453-703-6
; Sequence 6, Application US/08453703
; Patent No. 5768939
; GENERAL INFORMATION:
; APPLICANT: Conneely, Orla M.
; APPLICANT: Heaton, Denis R.
; APPLICANT: O'Malley, Bert W.
; APPLICANT: May, Gregory S.
; TITLE OF INVENTION: Production of Recombinant Lactoferrin
; TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-453-703-6

Query Match 80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 1,1e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSLDGF 23
Db 390 TTEDCIQVLKGEADAMSLDGF 412

RESULT 15
US-08-456-106-6
Sequence 6, Application US/08456106
Patent No. 5849881
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,106
FILING DATE: Concurrently herewith
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-106-6

Query Match 80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 1,1e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSLDGF 23
Db 390 TTEDCIQVLKGEADAMSLDGF 412

Search completed: June 13, 2006, 04:25:49
Job time : 40.5882 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:24 ; Search time 132.25 Seconds
(without alignments)
80.559 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 1 TTEDSIKINNGEADAMSLDGF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main.*

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2: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	23	4	US-10-612-162-2
2	110	95.7	328	3	US-09-891-126-5
3	110	95.7	328	4	US-10-266-745-5
4	110	95.7	679	4	US-10-378-094-3
5	110	95.7	679	4	US-10-384-060-3
6	110	95.7	679	4	US-10-231-494-3
7	110	95.7	679	5	US-10-429-482-4
8	110	95.7	679	5	US-10-429-487-4
9	110	95.7	679	5	US-10-429-515-4
10	110	95.7	679	5	US-10-429-598-4
11	110	95.7	679	5	US-10-429-635-4
12	110	95.7	679	5	US-10-429-653-4
13	110	95.7	679	5	US-10-429-659-4
14	110	95.7	679	5	US-10-429-661-4
15	110	95.7	679	5	US-10-429-660-4
16	110	95.7	679	5	US-10-429-662-4
17	110	95.7	679	5	US-10-429-654-4
18	110	95.7	679	5	US-10-429-654-4
19	110	95.7	698	3	US-09-935-642-6
20	110	95.7	698	4	US-10-378-094-2
21	110	95.7	698	4	US-10-384-060-2
22	110	95.7	698	4	US-10-231-494-2
23	110	95.7	698	4	US-10-383-201-10
24	110	95.7	698	4	US-10-383-201-14
25	110	95.7	698	5	US-10-887-711-2
26	110	95.7	698	5	US-10-513-523-3
27	110	95.7	698	6	US-11-177-506-46

28	110	95.7	698	6	US-11-038-901-2	Sequence 2, Appli
29	110	95.7	1074	3	US-09-753-385-2	Sequence 2, Appli
30	110	95.7	1410	3	US-09-753-385-4	Sequence 4, Appli
31	110	95.7	1410	5	US-10-473-127-805	Sequence 805, App
32	110	95.7	1418	5	US-10-473-127-804	Sequence 804, App
33	92	80.0	703	5	US-10-620-256-6	Sequence 6, Appli
34	92	80.0	704	5	US-10-513-523-3	Sequence 4, Appli
35	90	78.3	359	4	US-10-169-237-49	Sequence 49, Appli
36	90	78.3	690	4	US-10-076-816-4	Sequence 4, Appli
37	90	78.3	690	4	US-10-077-381-4	Sequence 4, Appli
38	90	78.3	690	4	US-10-639-835-4	Sequence 2, Appli
39	90	78.3	694	4	US-10-023-096-2	Sequence 273, App
40	90	78.3	695	4	US-10-316-253-273	Sequence 275, App
41	90	78.3	698	4	US-10-316-253-275	Sequence 55, Appli
42	90	78.3	698	4	US-10-205-331-55	Sequence 2, Appli
43	90	78.3	709	4	US-10-170-221-2	Sequence 2, Appli
44	90	78.3	709	5	US-10-987-587-2	Sequence 9, Appli
45	90	78.3	711	4	US-10-169-297-9	

ALIGNMENTS

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RESULT 1
US-10-612-162-2
; Sequence 2, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT FILING DATE: 2003-07-03
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-2

Query Match      100.0%; Score 115; DB 4; Length 23;
Best local similarity 100.0%; Pred. No. 6, 2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  TTEDSIKINNGEADAMSLDGF 23
Db      1  TTEDSIKINNGEADAMSLDGF 23

RESULT 2
US-09-891-126-5
; Sequence 5, Application US/09891126
; Patent No. US20020072596A1
; GENERAL INFORMATION:
; APPLICANT: Ruden et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035P1
; CURRENT FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-126-5
Query Match      95.7%; Score 110; DB 3; Length 328;
Best Local Similarity 95.7%; Pred. No. 8,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 56 TTEDCIKINNGEADAMSLDGCF 78

RESULT 3
US-10-266-745-5
; Sequence 5, Application US/10266745
; Publication No. US20030149256A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035PI
; CURRENT APPLICATION NUMBER: US/10/266,745
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-745-5

Query Match      95.7%; Score 110; DB 4; Length 328;
Best Local Similarity 95.7%; Pred. No. 8,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 56 TTEDCIKINNGEADAMSLDGCF 78

RESULT 4
US-10-378-094-3
; Sequence 3, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
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; OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3
Query Match      95.7%; Score 110; DB 4; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 373 TTEDCIKINNGEADAMSLDGCF 395

RESULT 5
US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match      95.7%; Score 110; DB 4; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
Db 373 TTEDCIKINNGEADAMSLDGCF 395

RESULT 6
US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3

Query Match 95.7%; Score 110; DB 4; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSIDGCF 23
DB 373 TTEDCIKINMGADAMSIDGCF 395

RESULT 7
US-10-429-482-4

Sequence 4, Application US/10429482
Publication No. US20040219097A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tu
FILE REFERENCE: 2537.000001
CURRENT APPLICATION NUMBER: US/10/429,482
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-482-4

Query Match 95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSIDGCF 23
DB 373 TTEDCIKINMGADAMSIDGCF 395

RESULT 8
US-10-429-497-4

Sequence 4, Application US/10429497
Publication No. US20040219098A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Methods For The Treatment of Tumors
FILE REFERENCE: 2537.000006
CURRENT APPLICATION NUMBER: US/10/429,497
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-497-4

Query Match 95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSIDGCF 23
DB 373 TTEDCIKINMGADAMSIDGCF 395

RESULT 9
US-10-429-515-4

Sequence 4, Application US/10429515
Publication No. US20040219099A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Methods For The Treatment Of Tumors

FILE REFERENCE: 2537.000005
CURRENT APPLICATION NUMBER: US/10/429,515
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-515-4

Query Match 95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSIDGCF 23
DB 373 TTEDCIKINMGADAMSIDGCF 395

RESULT 10
US-10-429-598-4

Sequence 4, Application US/10429598
Publication No. US20040219100A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Composition Useful For The Treatment of Tumors
FILE REFERENCE: 2537.000003
CURRENT APPLICATION NUMBER: US/10/429,598
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-598-4

Query Match 95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSIDGCF 23
DB 373 TTEDCIKINMGADAMSIDGCF 395

RESULT 11
US-10-429-635-4

Sequence 4, Application US/10429635
Publication No. US20040219101A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
FILE REFERENCE: 2537.000007
CURRENT APPLICATION NUMBER: US/10/429,635
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-635-4

Query Match 95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSIDGCF 23
DB 373 TTEDCIKINMGADAMSIDGCF 395

```
RESULT 12
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4
```

```
Query Match          95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKINNGEADAMSLDGCF 23
DB 373 TTEDCIKINNGEADAMSLDGCF 395
```

```
RESULT 13
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4
```

```
Query Match          95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 TTEDSIKINNGEADAMSLDGCF 23
DB 373 TTEDCIKINNGEADAMSLDGCF 395
```

```
RESULT 14
US-10-429-661-4
; Sequence 4, Application US/10429661
; Publication No. US20040219104A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Treatment Of Tumors
; FILE REFERENCE: 2537.000008
; CURRENT APPLICATION NUMBER: US/10/429,661
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-661-4
```

```
Query Match          95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKINNGEADAMSLDGCF 23
DB 373 TTEDCIKINNGEADAMSLDGCF 395
```

```
RESULT 15
US-10-429-660-4
; Sequence 4, Application US/10429660
; Publication No. US20040220084A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Nucleic Acid Delivery
; FILE REFERENCE: 2537.000012
; CURRENT APPLICATION NUMBER: US/10/429,660
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-660-4
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Query Match          95.7%; Score 110; DB 5; Length 679;
Best Local Similarity 95.7%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 TTEDSIKINNGEADAMSLDGCF 23
DB 373 TTEDCIKINNGEADAMSLDGCF 395
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Search completed: June 13, 2006, 04:56:24
Job time : 132.25 secs
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:58 ; Search time 7.77941 Seconds
(without alignments)
37.380 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSIKIMNGEADAMSLDGPF 23

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	95.7	679	6	US-10-515-429-3 Sequence 3, Appli
2	110	95.7	698	6	US-10-515-429-2 Sequence 2, Appli
3	101	87.8	676	6	US-10-515-429-37 Sequence 37, Appli
4	96	83.5	688	6	US-10-515-429-40 Sequence 40, Appli
5	92	80.0	677	6	US-10-515-429-39 Sequence 39, Appli
6	92	80.0	685	6	US-10-515-429-41 Sequence 41, Appli
7	92	80.0	686	6	US-11-258-767-36 Sequence 36, Appli
8	92	80.0	686	6	US-10-515-429-42 Sequence 42, Appli
9	92	80.0	703	7	US-11-258-767-37 Sequence 37, Appli
10	90	78.3	676	6	US-10-515-429-38 Sequence 38, Appli
11	90	78.3	698	7	US-11-258-767-25 Sequence 25, Appli
12	90	78.3	709	7	US-11-258-767-31 Sequence 31, Appli
13	90	78.3	710	7	US-11-258-767-33 Sequence 33, Appli
14	90	78.3	711	7	US-11-258-767-12 Sequence 12, Appli
15	90	78.3	711	7	US-11-258-767-15 Sequence 15, Appli
16	90	78.3	711	7	US-11-258-767-17 Sequence 17, Appli
17	90	78.3	711	7	US-11-258-767-18 Sequence 18, Appli
18	90	78.3	711	7	US-11-258-767-21 Sequence 21, Appli
19	90	78.3	711	7	US-11-258-767-27 Sequence 27, Appli
20	90	78.3	711	7	US-11-258-767-30 Sequence 30, Appli
21	88	76.5	707	7	US-11-258-767-14 Sequence 14, Appli
22	88	76.5	707	7	US-11-258-767-20 Sequence 20, Appli
23	87	75.7	708	7	US-11-258-767-23 Sequence 23, Appli
24	87	75.7	708	7	US-11-258-767-24 Sequence 24, Appli
25	84	73.0	708	7	US-11-258-767-19 Sequence 19, Appli

26	84	73.0	708	7	US-11-258-767-32 Sequence 32, Appli
27	83	72.2	695	7	US-11-258-767-26 Sequence 26, Appli
28	82	71.3	711	7	US-11-258-767-34 Sequence 34, Appli
29	77	67.0	681	7	US-11-258-767-13 Sequence 13, Appli
30	77	67.0	686	6	US-10-515-429-43 Sequence 43, Appli
31	77	67.0	708	7	US-11-258-767-16 Sequence 16, Appli
32	77	67.0	708	7	US-11-258-767-22 Sequence 22, Appli
33	77	67.0	708	7	US-11-258-767-28 Sequence 28, Appli
34	77	67.0	708	7	US-11-258-767-29 Sequence 29, Appli
35	77	67.0	708	7	US-11-258-767-35 Sequence 35, Appli
36	77	67.0	708	7	US-11-258-767-38 Sequence 38, Appli
37	77	67.0	708	7	US-11-258-767-39 Sequence 39, Appli
38	45	39.1	325	6	US-10-520-999-10 Sequence 10, Appli
39	45	39.1	333	6	US-10-520-999-9 Sequence 9, Appli
40	45	39.1	342	6	US-10-515-429-63 Sequence 63, Appli
41	45	39.1	451	6	US-10-520-999-8 Sequence 8, Appli
42	45	39.1	530	6	US-10-520-999-12 Sequence 12, Appli
43	44	38.3	1100	6	US-10-953-349-1942 Sequence 1942, Ap
44	44	38.3	1151	6	US-10-953-349-1941 Sequence 1941, Ap

ALIGNMENTS

```
RESULT 1
US-10-515-429-3
; Sequence 3, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Christopher P.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
US-10-515-429-3
Query Match          95.7%; Score 110; DB 6; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy      1  TTEDSIKIMNGEADAMSLDGPF 23
Db      373 TTEDSIKIMNGEADAMSLDGPF 395
RESULT 2
US-10-515-429-2
; Sequence 2, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
```

```
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 698
TYPE: PRT
ORGANISM: Homo sapiens
US-10-515-429-2
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```
Query Match      95.7%; Score 110; DB 6; Length 698;
Best Local Similarity 95.7%; Pred. No. 1,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 TTEDSIKINNGEADAMSLDGGF 23
Db      392 TTEDCIKIVKGADAMSLDGGF 414
```

RESULT 3

```
US-10-515-429-37
Sequence 37, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 676
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-10-515-429-37
```

```
Query Match      87.8%; Score 101; DB 6; Length 676;
Best Local Similarity 87.8%; Pred. No. 3,4e-08;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 TTEDSIKINNGEADAMSLDGGF 23
Db      373 TPEDCIKINNGEADAMSLDGGY 395
```

RESULT 4

```
US-10-515-429-40
Sequence 40, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun
```

```
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 688
TYPE: PRT
ORGANISM: Equus caballus
US-10-515-429-40
```

```
Query Match      83.5%; Score 96; DB 6; Length 688;
Best Local Similarity 82.6%; Pred. No. 2e-07;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 TTEDSIKINNGEADAMSLDGGF 23
Db      376 STEDCIKIVKGADAMSLDGGF 398
```

RESULT 5

```
US-10-515-429-39
Sequence 39, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 39
LENGTH: 677
TYPE: PRT
ORGANISM: Mus musculus
US-10-515-429-39
```

```
Query Match      80.0%; Score 92; DB 6; Length 677;
Best Local Similarity 81.8%; Pred. No. 8,4e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 TTEDSIKINNGEADAMSLDGG 22
Db      372 TTEDCIKIVKGADAMSLDGG 393
```

RESULT 6

```
US-10-515-429-41
Sequence 41, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
```

```

; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-515-429-41
```

```

Query Match          80.0%; Score 92; DB 6; Length 685;
Best Local Similarity 81.8%; Pred. No. 8.5e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 TEDSIKIMNGEADAMSLDGGF 23
```

```
Db      377 TEECIAKIMNGEADAMSLDGGY 398
```

```

RESULT 7
US-11-258-767-36
; Sequence 36, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 686
; TYPE: PRT
; ORGANISM: PIG
US-11-258-767-36
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Query Match          80.0%; Score 92; DB 7; Length 686;
Best Local Similarity 73.9%; Pred. No. 8.5e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 TTEDSIKIMNGEADAMSLDGGF 23
```

```
Db      391 TTEDCIYQVLKGEADAMSLDGGF 413
```

```

RESULT 8
US-10-515-429-42
; Sequence 42, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
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; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (308)..(308)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-515-429-42
```

```

Query Match          80.0%; Score 92; DB 6; Length 696;
Best Local Similarity 81.8%; Pred. No. 8.7e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 TEDSIKIMNGEADAMSLDGGF 23
```

```
Db      378 TEDCIAKIMNGEADAMSLDGGY 399
```

```

RESULT 9
US-11-258-767-37
; Sequence 37, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 703
; TYPE: PRT
; ORGANISM: PIG
US-11-258-767-37
```

```

Query Match          80.0%; Score 92; DB 7; Length 703;
Best Local Similarity 73.9%; Pred. No. 8.8e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 TTEDSIKIMNGEADAMSLDGGF 23
```

```
Db      390 TTEDCIYQVLKGEADAMSLDGGF 412
```

```

RESULT 10
US-10-515-429-38
; Sequence 38, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
```

```
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-515-429-38
```

```
Query Match      78.3%; Score 90; DB 6; Length 676;
Best Local Similarity 81.8%; Pred. No. 1.7e-06;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TTEDSIKINNGEADAMSIDGG 22
Db      369 STEDCIDKIVNGEADAMSIDGG 390
```

```
RESULT 11
US-11-258-767-25
; Sequence 25, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 698
; TYPE: PRT
; ORGANISM: RAT
; US-11-258-767-25
```

```
Query Match      78.3%; Score 90; DB 7; Length 698;
Best Local Similarity 81.8%; Pred. No. 1.8e-06;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TTEDSIKINNGEADAMSIDGG 22
Db      391 STEDCIDKIVNGEADAMSIDGG 412
```

```
RESULT 12
US-11-258-767-31
; Sequence 31, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
```

```
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 709
; TYPE: PRT
; ORGANISM: HUMAN
; US-11-258-767-31
```

```
Query Match      78.3%; Score 90; DB 7; Length 709;
Best Local Similarity 73.9%; Pred. No. 1.8e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 TTEDSIKINNGEADAMSIDGGF 23
Db      394 TTEDCIATLVKGEADAMSIDGGY 416
```

```
RESULT 13
US-11-258-767-33
; Sequence 33, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 710
; TYPE: PRT
; ORGANISM: HUMAN
; US-11-258-767-33
```

```
Query Match      78.3%; Score 90; DB 7; Length 710;
Best Local Similarity 73.9%; Pred. No. 1.8e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 TTEDSIKINNGEADAMSIDGGF 23
Db      395 TTEDCIATLVKGEADAMSIDGGY 417
```

```
RESULT 14
US-11-258-767-12
; Sequence 12, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
; US-11-258-767-12
```

```
Query Match      78.3%; Score 90; DB 7; Length 711;
```

Best Local Similarity 73.9%; Pred. No. 1.8e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
||| | : ||| | ||| |
Db 396 TTEDCIALVLKGEADAMSLDGCF 418

RESULT 15
US-11-258-767-15
; Sequence 15, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P0291SUS1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent version 3.3
; SEQ ID NO 15
; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-15

Query Match 78.3%; Score 90; DB 7; Length 711;
Best Local Similarity 73.9%; Pred. No. 1.8e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSLDGCF 23
||| | : ||| | ||| |
Db 396 TTEDCIALVLKGEADAMSLDGCF 418

Search completed: June 13, 2006, 04:56:53
Job time : 7.77941 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:00:59 ; Search time 194 Seconds
(without alignments)
54.206 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSTAKIMNGEADMSLDGFG 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 12745

Minimum DB seq length: 23
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003s:*
- 7: geneseqp2004s:*
- 8: geneseqp2005s:*
- 9: geneseqp2006s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	23	8 ADG46076	ADG46076 Human CDT
2	82	71.3	23	10 AEB39174	Aeb39174 Human ser
3	32	27.8	23	9 ADZ86384	Adz86384 Protein q
4	32	27.8	23	9 AEB25314	Aeb25314 Synthetic
5	32	27.8	23	9 AEC83228	Aec83228 Peptide d
6	30	26.1	23	9 ADV12367	Adv12367 Human pho
7	29	25.2	23	8 ADK49860	Adk49860 Human car
8	28	24.3	23	10 AEF54127	Aef54127 N. mening
9	27	23.5	23	4 AAG63463	Aag63463 Amino aci
10	27	23.5	23	4 AAG63471	Aag63471 Amino aci
11	27	23.5	23	4 AAG63466	Aag63466 Amino aci
12	27	23.5	23	4 AAG63470	Aag63470 Amino aci
13	27	23.5	23	4 AAG63473	Aag63473 Amino aci
14	27	23.5	23	4 AAG63465	Aag63465 Amino aci
15	27	23.5	23	4 AAG63468	Aag63468 Amino aci
16	27	23.5	23	4 AAG63475	Aag63475 Amino aci
17	27	23.5	23	4 AAG63458	Aag63458 Amino aci
18	27	23.5	23	4 AAG63460	Aag63460 Amino aci
19	27	23.5	23	4 AAG63461	Aag63461 Amino aci
20	27	23.5	23	4 AAG63476	Aag63476 Amino aci
21	27	23.5	23	4 AAU32268	AAu32268 Novel hum
22	27	23.5	23	5 ABG95983	ABg95983 Cysteine-
23	27	23.5	23	7 ABR62927	ABr62927 Bovine se

24	27	23.5	23	7 ADE01183	AdE01183 Bovine Se
25	27	23.5	23	7 ADF51339	AdF51339 Antiangio
26	27	23.5	23	7 AEB21274	Aeb21274 Amino aci
27	27	23.5	23	9 ADV50385	Adv50385 Cysteine-
28	27	23.5	23	9 AEB25313	Aeb25313 Synthetic
29	27	23.5	23	10 AEF76775	Aef76775 Synchrocy
30	26.5	23.0	23	8 ADK50301	Adk50301 Human car
31	26	22.6	23	2 AAW74556	Aaw74556 N-termina
32	26	22.6	23	4 AAG63477	Aag63477 Amino aci
33	26	22.6	23	4 AAG63459	Aag63459 Amino aci
34	26	22.6	23	4 AAG63469	Aag63469 Amino aci
35	26	22.6	23	4 AAG63462	Aag63462 Amino aci
36	26	22.6	23	4 AAG63472	Aag63472 Amino aci
37	26	22.6	23	4 AAG63464	Aag63464 Amino aci
38	26	22.6	23	4 AAG63474	Aag63474 Amino aci
39	26	22.6	23	4 AAG63467	Aag63467 Amino aci
40	26	22.6	23	5 ABG32088	ABg32088 Cryptospor
41	26	22.6	23	7 ADD88708	Add88708 Malarial
42	26	22.6	23	7 ADG38473	Adg38473 P. falcip
43	26	22.6	23	9 ADV52893	Adv52893 Hedgehog
44	26	22.6	23	9 ADW92635	ADw92635 P. falcip
45	25	21.7	23	2 AAR54368	Aar54368 RAE 70.1-

ALIGNMENTS

RESULT 1
ADG46076
ID ADG46076 standard; peptide; 23 AA.
XX
AC ADG46076;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #2.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN BPJ378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003BP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
XX Claim 4; SEQ ID NO 2; 21bp; German.
XX
PS This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences VVARSWGKEDLIWELL, TTEDSTAKIMNGEADMSLDGFG, STLSMGSLNLEPN and
XX YERYLDEYVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for

CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC acetalolols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilizing it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 115; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTEDSIATKINGEADAMSLDGGF 23
1 TTEDSIATKINGEADAMSLDGGF 23

Db 1 TTEDSIATKINGEADAMSLDGGF 23

RESULT 2
AEE39174
ID AEE39174 standard; peptide; 23 AA.
XX
AC AEE39174;
XX
DT 09-FEB-2006 (first entry)
XX
DE Human serum N-linked glycopeptide SEQ ID NO: 3278.
XX
KM Bioinformatics; blood; serum; plasma protein; protein detection;
KM mass spectrometry; proteomics; glycosylation; diagnosis; cancer;
KM cyrostatic; diabetes; antidiabetic; inflammation; antiinflammacy;
KM rheumatoid arthritis; antiarthritic; antirheumatic; psychiatric disorder;
KM neuroleptic; neurological disease; infection; antimicrobial.

XX
OS Homo sapiens.
XX
PN WO2005114221-A2.
XX
PD 01-DEC-2005.
XX
PF 20-MAY-2005; 2005WO-US017842.
XX
PR 21-MAY-2004; 2004US-0573593P.
XX
PA (SYST-) INST SYSTEMS BIOLOGY.
XX
PI Aebersold RH, Zhang H;
XX
DR WPI; 2006-020173/02.
XX
PT Identifying glycopolypeptides in a serum or plasma sample, by identifying
PT released sample glycopeptide fragments that correspond to standard
PT peptides.

XX
PS Claim 1; SEQ ID NO 3278; 193pp; English.

XX
XX The invention relates to identifying glycopolypeptides in a serum or
CC plasma sample comprising immobilizing derivatized sample
CC glycopolypeptides to a solid support, releasing the sample glycopeptide
CC fragments from the solid support, adding to the released sample
CC glycopeptide fragments standard peptides, and identifying released sample
CC glycopeptide fragments that correspond to standard peptides added by mass
CC spectroscopy. Also included are a method for identifying one or more
CC diagnostic markers for a disease, a composition comprising peptides
CC containing the glycosylation sites (AEE35897-AEE39378), where the peptides
CC each correspond to peptide fragments derived by cleavage of polypeptides
CC using the same cleavage reagent) and a kit comprising peptides containing
CC the glycosylation sites (AEE35897-AEE39378). The methods are useful for
CC identifying glycopolypeptides in a serum or plasma sample. The methods
CC can be used for blood serum profiling for the detection of prognostic and
CC diagnostic protein markers. It can also be used to identify and/or
CC validate drug targets and to evaluate drug efficacy, drug dosing, and/or

CC drug toxicity. The methods can also be used for the detection of changes
CC in the state of glycosylation of proteins based on the concurrent
CC application of protein abundance measurement of protein glycosylation on
CC the same sample. The method allows fast throughput analysis of samples, which can be
CC be readily adapted for high throughput analysis of samples, which can be
CC particularly advantageous for the analysis of clinical specimens. The
CC method can also be automated to facilitate the processing of multiple
CC samples. The present sequence is a human glycopeptide that does not
CC contain an N-linked glycosylation site, suitable for use as a reference
CC peptide in the method of the invention.

XX
SQ Sequence 23 AA;

Query Match 71.3%; Score 82; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KINNGEADAMSLDGGF 23
1 KINNGEADAMSLDGGF 16

Db 1 KINNGEADAMSLDGGF 16

RESULT 3
AD286384
ID AD286384 standard; peptide; 23 AA.
XX
AC AD286384;
XX
DT 14-JUL-2005 (first entry)
XX
DE Protein quantitative analysis method related al drama peptide #11.
XX
KM quantitative analysis; HPLC; electrospray ionization; mass spectroscopy;
KM proteomics.

XX
OS Unidentified.
XX
PN JP2005121380-A.
XX
PD 12-MAY-2005.
XX
PF 14-OCT-2003; 2003JP-00353574.
XX
PR 14-OCT-2003; 2003JP-00353574.
XX
PA (SUMO) SUMITOMO SEIYAKU KK.
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
DR WPI; 2005-349932/36.
XX
PT Quantitative analysis of protein, by hydrolyzing test sample and control
PT in water containing labeled oxygen, mixing hydrolyzed substance and
PT subjecting liquid mixture to liquid chromatography/electrospray
PT ionization-mass spectrometry.

XX
PS Example 3; Page; 13pp; Japanese.

XX
XX The invention relates to a novel method for the quantitative analysis of
CC a protein. The method involves hydrolyzing a first test sample in water
CC containing 90% or more of 18-O (an isotopic labeling element),
CC hydrolyzing a second sample in water containing 90% or more of 16-O,
CC mixing the hydrolyzed substance of the first and second samples, and
CC carrying out quantitative analysis of the liquid mixture by liquid
CC chromatography/electrospray ionization-mass spectrometry (LC/ESI-MS). The
CC method enables the quantification of proteins in large-scale proteomics,
CC and trace amount of proteins present in an organism can be quantified
CC accurately and efficiently. This sequence represents a peptide fragment
CC used in the protein quantitative analysis method of the invention.

XX
SQ Sequence 23 AA;

Query Match 27.8%; Score 32; DB 9; Length 23;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;

[illegible]

DE	Peptide derived from Aldolase A, fructose-bisphosphate ALDOA, seqid 13.
KM	contraceptive; pharmaceutical; antibody therapy; diagnosis; infertility;
KW	antinfertility; genitourinary disease; Aldolase A;
KW	fructose bisphosphate ALDOA.
XX	
OS	Homo sapiens.
PM	WO2005089429-A2.
PD	
29-SEP-2005.	
PF	17-MAR-2005; 2005WO-US0008906.
XX	
PR	17-MAR-2004; 2004US-0554085P.
PR	30-SEP-2004; 2004US-0614817P.
XX	
PA	(UNIV-) UNIV VIRGINIA PATENT FOUND.
XX	
PI	Kim Y, Herr JC;
DR	WPI; 2005-649557/66.
XX	
PT	New mammalian sperm flagellar energy carrier (SPEC) protein, its homolog,
PT	derivative or fragment, useful as contraceptive, and for treating sperm
PT	flagellar energy carrier protein-associated disease or disorder, e.g.
PT	infertility.
PS	Disclosure; Fig 8; 80pp; English.
XX	
XX	
CC	The new invention relates to a new mammalian sperm specific fibrous
CC	sheath protein, that is believed to function as an adenine nucleotide
CC	translocase, and has been designated sperm flagellar energy carrier
CC	(SPEC) protein comprising SEQ ID NO: 2 or 4. The protein is located in
CC	the principle piece of the sperm tail, but not in the midpiece. SPEC is
CC	believed to be essential for sperm motility, and thus antagonists of SPEC
CC	may have use as contraceptive agents. Also claimed are a pharmaceutical
CC	composition comprising the sperm flagellar energy carrier protein, and a
CC	carrier; an isolated nucleic acid encoding the sperm flagellar energy
CC	carrier protein; a vector comprising the nucleic acid; a host cell
CC	comprising the vector; a composition comprising an isolated nucleic acid
CC	complementary to a nucleic acid encoding a sperm flagellar energy carrier
CC	protein, and a carrier; an antibody that binds to a sperm flagellar
CC	energy carrier protein; a pharmaceutical composition comprising the
CC	antibody, and a carrier; an antigenic composition comprising a protein
CC	having SEQ ID NO: 2; and a carrier; a method of diagnosing a sperm
CC	flagellar energy carrier protein-associated disease or disorder related
CC	to aberrant sperm flagellar energy carrier protein expression, function,
CC	or levels; and a method of treating a sperm flagellar energy carrier
CC	protein-associated disease or disorder; a method of regulating sperm
CC	flagellar energy carrier protein expression, function, or levels in a
CC	subject. The sperm flagellar energy carrier protein is useful for
CC	treating sperm flagellar energy carrier protein-associated disease or
CC	disorder, e.g. infertility. The protein is also useful as contraceptive
CC	agent. The present sequence is a peptide derived from human Aldolase A,
CC	fructose-bisphosphate ALDOA.
XX	
XX	
SQ	Sequence 23 AA;
QY	Query Match 27.8%; Score 32; DB 9; Length 23;
Db	Best Local Similarity 54.5%; Pred. No. 9.4e+02;
	Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0.
	11 NGEADAMSLDG 21
	9 NGETTGGLDG 19
RESULT 6	
ADV12367	
ID	ADV12367 standard; peptide; 23 AA.
AC	ADV12367;

XX 10-MAR-2005 (first entry)
 DT Human phosphorylated peptide from phosphoprotein #305.
 XX
 XX Alzheimer's disease; neuroprotective; neurotrophic; degeneration; tumor;
 KM neoplasm; neurological disease; phosphorylation; protein sequencing;
 KM phosphoprotein.
 XX
 XX Homo sapiens.
 OS
 XX MO2004108948-A2.
 PN
 XX 16-DEC-2004.
 PD
 XX 04-JUN-2004; 2004WO-US017613.
 PF
 XX 04-JUN-2003; 2003US-0476010P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Gysi SP;
 PI
 XX WPI; 2005-031720/03.
 DR
 XX
 XX Characterizing phosphorylated polypeptides in a sample comprises
 PT digesting the polypeptides with a protease thus generating test peptides,
 PT and collecting a fraction of test peptides that enriched for positively
 PT charged peptides.
 XX
 XX Claim 16; Page 69; 123pp; English.
 PS
 XX The invention relates to characterizing phosphorylated polypeptides in a
 CC sample comprising digesting the polypeptides with a protease thus
 CC generating test peptides, and collecting a fraction of test peptides that
 CC enriched for positively charged peptides. Also included are a method
 CC (comprising determining the presence, absence or level of one or more
 CC phosphorylated peptides as identified above in cells having a cell strata
 CC and determining the degree of correlation between the presence, absence
 CC or level of phosphorylated polypeptide with the cell strata), an isolated
 CC peptide of 5-50 amino acids comprising an amino acid sequence that is a
 CC subsequence of any of the protein sequences given in the specification
 CC (and which comprise a phosphorylation site within the subsequence), an
 CC isolated polypeptide selected from any of the polypeptides listed in the
 CC specification and is modified at a modification site, an isolated peptide
 CC comprising a mass spectral peak signatures, a method for identifying a
 CC treatment that modulates phosphorylation of an amino acid in a target
 CC polypeptide, a method for generating a peptide standard, a pair of
 CC peptide standards comprising the peptide obtained (where the peptide is
 CC phosphorylated and a corresponding peptide comprising an identical amino
 CC acid sequence but which is not phosphorylated), a system (comprising a
 CC computer memory comprising data files storing information relating to the
 CC identifying characteristics of positively charged peptides), and a data
 CC analysis module capable of executing instructions for organizing and/or
 CC searching the data files), a computer program product (comprising data
 CC relating to the identifying characteristics of positively charged
 CC peptides and comprising instructions for organizing and/or searching the
 CC data), and a method for identifying N-terminal peptides in a sample. The
 CC method is useful for characterizing phosphorylated polypeptides in a
 CC sample. The present sequence is a peptide from a human phosphoprotein,
 CC containing a phosphorylation site, identified by the method of the
 CC invention.
 XX
 XX Sequence 23 AA;
 SQ
 Query Match 26.1%; Score 30; DB 9; Length 23;
 Best Local Similarity 54.5%; Pred. No. 2e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
 ADK49860
 ID ADK49860 standard; peptide; 23 AA.
 XX
 XX ADK49860;
 AC
 XX 04-NOV-2004 (first entry)
 DT
 XX Human carcinoma-related C35 epitope / gp100 Pmel17 polypeptide 751.
 DE
 XX C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma;
 KM human; polypeptide; gp100 Pmel17.
 KM
 XX Homo sapiens.
 OS
 XX Unidentified.
 OS
 XX WO2003104428-A2.
 PN
 XX 18-DEC-2003.
 PD
 XX 10-JUN-2003; 2003WO-US018252.
 PF
 XX 10-JUN-2002; 2002US-0386738P.
 PR 11-DEC-2002; 2002US-0432241P.
 PR 23-APR-2003; 2003US-0464650P.
 XX
 XX (VACC-) VACCINEX INC.
 PA (UVRP) UNIV ROCHESTER.
 PA
 PI Zauderer M, Evans EE, Borrello MA;
 XX
 XX WPI; 2004-062349/06.
 DR
 XX Novel C35 polypeptide useful for formulation of immunogenic composition
 PT to induce antibodies and cell-mediated immunity against tumor cells.
 PT
 XX Disclosure; Page 148; 626pp; English.
 PS
 XX The invention relates to a novel isolated polypeptide comprising or
 CC consisting of two or more C35 peptide epitopes. The polypeptide of the
 CC invention demonstrates cytostatic activity and may be useful for the
 CC formulation of an immunogenic composition, such as a vaccine, to induce
 CC antibodies and cell-mediated immunity against target cells such as tumor
 CC cells. Furthermore, the polypeptide and its analogues may be useful as
 CC prognostic markers for carcinoma, such as human breast or bladder
 CC carcinoma. The current sequence is that of human breast/bladder carcinoma
 CC C35 polypeptide of the invention.
 CC
 XX Sequence 23 AA;
 SQ
 Query Match 25.2%; Score 29; DB 8; Length 23;
 Best Local Similarity 35.3%; Pred. No. 2.8e+03;
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 5 STAKINNGEADAMSLDG 21
 1 TLKRTNSRPPCVLLDG 17

RESULT 8
 AEF54127
 ID AEF54127 standard; peptide; 23 AA.
 XX
 XX AEF54127;
 AC
 XX 23-MAR-2006 (first entry)
 DT
 XX N. meningitidis 2996 adhesin NadA HR2a extended SEQ ID NO:30.
 DE
 XX therapeutic; prophylaxis; nisseria meningitidis infection;
 KM haemophilus influenzae infection; antibacterial; adhesin; NadA.
 KM
 XX

OS Neisseria meningitidis.
 XX WO2006006074-A2.
 PN
 XX
 PD 19-JAN-2006.
 XX
 PF 06-JUL-2005; 2005WO-IB002320.
 XX
 PR 06-JUL-2004; 2004GB-00015160.
 XX
 PA (CHIR) CHIRON SRL.
 XX
 PI Maignant V;
 XX
 DR WPI; 2006-100915/10.
 XX
 PT New compound that binds to heptad repeat sequences HR1 or HR2 of Nada and
 PT Hada adhesin on the surface of meningococcus and haemophilus, useful for
 PT treating meningococcal or haemophilus infection.
 PS
 PS Claim 9; SEQ ID NO 30; 39pp; English.
 XX
 CC The invention relates to a compound that can bind to the heptad repeat
 CC sequences HR1 and/or HR2 of the Nada and Hada adhesin on the surface of a
 CC meningococcus and haemophilus, respectively, thus inhibiting the ability
 CC of the meningococcus and haemophilus either to infect a host organism or
 CC to spread an existing infection. The compound is an oligopeptide or
 CC polypeptide, or a peptidomimetic compound of the oligopeptide, with anti-
 CC meningococcal and/or anti-haemophilus activity. The invention also
 CC includes a pharmaceutical composition comprising the compound and a
 CC carrier; a method for treating a patient suffering from a meningococcal
 CC or haemophilus infection by administering to the patient the
 CC pharmaceutical composition; mutant Nada and Hada proteins, where the
 CC mutant protein lacks one or more of the HR1, HR2, or fusion sequences; a
 CC nucleic acid encoding the mutant protein; and a bacterium, which
 CC expresses the nucleic acid. The compound is useful as a medicament, for
 CC the manufacture of a medicament, and for treating a patient for
 CC meningococcal or haemophilus infection. This sequence is an extended
 CC Neisseria meningitidis 2996 adhesin Nada heptad repeat sequence HR2a.
 XX
 SQ Sequence 23 AA;
 Query Match 24.3%; Score 28; DB 10; Length 23;
 Best Local Similarity 54.5%; Pred. No. 4.1e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTEDSIKIMN 11
 Db 6 TNKDNIAKKAN 16
 RESULT 9
 AAG63463
 ID AAG63463 standard; peptide: 23 AA.
 XX
 AC AAG63463;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE Amino acid sequence of a peptide which is used in therapy.
 XX
 KW Haematopoiesis; haematopoietic stem cell; cell differentiation;
 KW haematopoiesis proliferative syndrome; cytoprotection;
 KW apoptosis; medullar expansion; inflammation; angiogenesis; myelofibrosis;
 KW thrombocytemia; Vasquez polyglobulia; chronic leukocytic leukemia;
 KW antiviral.
 XX
 OS Synthetic.
 XX
 PN WO200146218-A2.
 XX
 PD 28-JUN-2001.
 XX

PF 14-DEC-2000; 2000WO-FR003532.
 XX
 PR 22-DEC-1999; 99FR-00016273.
 XX
 PA (VAIS-) INST VAISSEUX & DU SANG.
 XX
 PI Alemany M, Caen JP, Han ZC;
 XX
 DR WPI; 2001-488621/53.
 XX
 PT New sicoso-, tricoso- or pentacoso- to heptacosio-peptides, useful e.g.
 PT for stimulating hematopoietic stem cell proliferation after chemotherapy
 PT or radiotherapy or as antiinflammatory agents.
 XX
 PS Example; Page 15; 33pp; French.
 XX
 CC AAG63418-AAG63511 represent peptides which are used in therapy. The
 CC peptides are haematopoiesis inhibitors, haematopoietic stem cell
 CC proliferation stimulants, cell differentiation inducers, and chemokine
 CC antagonists. The peptides are used as a medicament for treating the
 CC harmful effects of chemotherapy on haematopoietic stem cells; inhibiting
 CC haematopoietic proliferation, in the treatment of myeloproliferative
 CC syndromes; cytoprotection against cytotoxic effects, especially in
 CC protection of hematopoietic cells against apoptosis; medullar expansion
 CC or puting, in the treatment of medullar insufficiency or medullar grafts
 CC ; treating inflammation; inhibiting pathological angiogenesis; or
 CC differentiating abnormal cells into healthy cells. They are also used for
 CC treatment of essential thrombocytemia, Vasquez polyglobulia,
 CC myelofibrosis and chronic leukocytic leukemia. The peptides also show
 CC some antiviral activity, and are antagonists of chemokines of the CXC
 CC type and subfamily ELR, especially IL-8, NAP2, groalpha, grobeta and
 CC grogamma
 XX
 SQ Sequence 23 AA;
 Query Match 23.5%; Score 27; DB 4; Length 23;
 Best Local Similarity 33.3%; Pred. No. 6e+03;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 2 TEDSIKIMNGEADMSL 19
 Db 5 TAOIATLTKNGQKISLEL 22
 RESULT 10
 AAG63471
 ID AAG63471 standard; peptide: 23 AA.
 XX
 AC AAG63471;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE Amino acid sequence of a peptide which is used in therapy.
 XX
 KW Haematopoiesis; haematopoietic stem cell; cell differentiation;
 KW haematopoiesis proliferative syndrome; cytoprotection;
 KW apoptosis; medullar expansion; inflammation; angiogenesis; myelofibrosis;
 KW thrombocytemia; Vasquez polyglobulia; chronic leukocytic leukemia;
 KW antiviral.
 XX
 OS Synthetic.
 XX
 PN WO200146218-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 14-DEC-2000; 2000WO-FR003532.
 XX
 PR 22-DEC-1999; 99FR-00016273.
 XX
 PA (VAIS-) INST VAISSEUX & DU SANG.
 XX
 PI Alemany M, Caen JP, Han ZC;
 XX

XX
DR WPI; 2001-488621/53.
XX
XX New eicosaa-, tricosaa- or pentacosaa- to heptacosaa-peptides, useful e.g.
PT for stimulating hematopoietic stem cell proliferation after chemotherapy
PT or radiotherapy or as antiinflammatory agents.
XX
XX Example; Page 15; 33pp; French.
XX
XX AAG63418-AAG63511 represent peptides which are used in therapy. The
CC peptides are hematopoiesis inhibitors, hematopoietic stem cell
CC proliferation stimulants, cell differentiation inducers, and chemokine
CC antagonists. The peptides are used as a medicament for treating the
CC harmful effects of chemotherapy on hematopoietic stem cells; inhibiting
CC hematopoietic proliferation, in the treatment of myeloproliferative
CC syndromes; cytoprotection against cytotoxic effects, especially in
CC protection of hematopoietic cells against apoptosis; medullar expansion
CC or purging, in the treatment of medullar insufficiency or medullar grafts
CC ; treating inflammation; inhibiting pathological angiogenesis; or
CC differentiating abnormal cells into healthy cells. They are also used for
CC treatment of essential thrombocytemia, Vaquez polyglobulia,
CC myelofibrosis and chronic leukocytic leukemia. The peptides also show
CC some antiviral activity, and are antagonists of chemokines of the CXC
CC type and subfamily ELR, especially IL-8, NAP2, groalpha, grobeta and
CC grogamma
XX
SQ Sequence 23 AA;
XX
XX
Query Match 23.5%; Score 27; DB 4; Length 23;
Best Local Similarity 35.7%; Pred. No. 6e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
QY 6 IAKINGEADAMSL 19
| : | : | : |
Db 9 IVLKNKGQKISLEL 22
XX
RESULT 11
AAG63466
ID AAG63466 standard; peptide; 23 AA.
XX
XX AAG63466;
XX
XX 15-OCT-2001 (first entry)
XX
XX Amino acid sequence of a peptide which is used in therapy.
XX
XX
XX Haematopoiesis; haematopoietic stem cell; cell differentiation;
KM haematopoiesis proliferation; myeloproliferative syndrome; cytoprotection;
KM apoptosis; medullar expansion; inflammation; angiogenesis; myelofibrosis;
KM thrombocytemia; Vaquez polyglobulia; chronic leukocytic leukemia;
KM antiviral.
XX
XX Synthetic.
XX
XX WO200146218-A2.
XX
XX 28-JUN-2001.
XX
XX 14-DEC-2000; 2000WO-FR003532.
XX
XX 22-DEC-1999; 99FR-00016273.
XX
XX (VAIS-) INST VAISSEAU & DU SANG.
XX
XX Alemany M, Caen JP, Han ZC;
XX
XX WPI; 2001-488621/53.
XX
XX New eicosaa-, tricosaa- or pentacosaa- to heptacosaa-peptides, useful e.g.
PT for stimulating hematopoietic stem cell proliferation after chemotherapy
PT or radiotherapy or as antiinflammatory agents.
XX

PS Example; Page 15; 33pp; French.
XX
XX AAG63418-AAG63511 represent peptides which are used in therapy. The
CC peptides are hematopoiesis inhibitors, hematopoietic stem cell
CC proliferation stimulants, cell differentiation inducers, and chemokine
CC antagonists. The peptides are used as a medicament for treating the
CC harmful effects of chemotherapy on hematopoietic stem cells; inhibiting
CC hematopoietic proliferation, in the treatment of myeloproliferative
CC syndromes; cytoprotection against cytotoxic effects, especially in
CC protection of hematopoietic cells against apoptosis; medullar expansion
CC or purging, in the treatment of medullar insufficiency or medullar grafts
CC ; treating inflammation; inhibiting pathological angiogenesis; or
CC differentiating abnormal cells into healthy cells. They are also used for
CC treatment of essential thrombocytemia, Vaquez polyglobulia,
CC myelofibrosis and chronic leukocytic leukemia. The peptides also show
CC some antiviral activity, and are antagonists of chemokines of the CXC
CC type and subfamily ELR, especially IL-8, NAP2, groalpha, grobeta and
CC grogamma
XX
SQ Sequence 23 AA;
XX
XX
Query Match 23.5%; Score 27; DB 4; Length 23;
Best Local Similarity 35.7%; Pred. No. 6e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
QY 6 IAKINGEADAMSL 19
| : | : | : |
Db 9 IVLKNKGQKISLEL 22
XX
RESULT 12
AAG63470
ID AAG63470 standard; peptide; 23 AA.
XX
XX AAG63470;
XX
XX 15-OCT-2001 (first entry)
XX
XX Amino acid sequence of a peptide which is used in therapy.
XX
XX
XX Haematopoiesis; haematopoietic stem cell; cell differentiation;
KM haematopoiesis proliferation; myeloproliferative syndrome; cytoprotection;
KM apoptosis; medullar expansion; inflammation; angiogenesis; myelofibrosis;
KM thrombocytemia; Vaquez polyglobulia; chronic leukocytic leukemia;
KM antiviral.
XX
XX Synthetic.
XX
XX WO200146218-A2.
XX
XX 28-JUN-2001.
XX
XX 14-DEC-2000; 2000WO-FR003532.
XX
XX 22-DEC-1999; 99FR-00016273.
XX
XX (VAIS-) INST VAISSEAU & DU SANG.
XX
XX Alemany M, Caen JP, Han ZC;
XX
XX WPI; 2001-488621/53.
XX
XX New eicosaa-, tricosaa- or pentacosaa- to heptacosaa-peptides, useful e.g.
PT for stimulating hematopoietic stem cell proliferation after chemotherapy
PT or radiotherapy or as antiinflammatory agents.
XX
XX Example; Page 15; 33pp; French.
XX
XX AAG63418-AAG63511 represent peptides which are used in therapy. The
CC peptides are hematopoiesis inhibitors, hematopoietic stem cell
CC proliferation stimulants, cell differentiation inducers, and chemokine
CC antagonists. The peptides are used as a medicament for treating the
CC harmful effects of chemotherapy on hematopoietic stem cells; inhibiting

Query Match 23.5%; Score 27; DB 4; Length 23;
 Best Local Similarity 33.3%; Pred. No. 6e+03;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Search completed: June 13, 2006, 02:04:22
 Job time : 196 secs

QY 2 TEDSIKINNGEADAMSL 19
 | : : : : :
 5 TAQLIATLKNQKISLEL 22

RESULT 15

AA63468
 ID AA63468 standard; peptide; 23 AA.

XX AA63468;

DT 15-OCT-2001 (first entry)

DE Amino acid sequence of a peptide which is used in therapy.

XX Haematopoiesis; haematopoietic stem cell; cell differentiation;

KM haematopoiesis proliferation; myeloproliferative syndrome; cytoprotection;

KW apoptosis; medullar expansion; inflammation; angiogenesis; myelofibrosis;

KM thrombocytopenia; Vaequez polyglobulia; chronic leukocytic leukemia;

XX antiviral.

XX Synthetic.

PN WO200146218-A2.

PD 28-JUN-2001.

XX 14-DEC-2000; 2000WO-FR003532.

XX 22-DEC-1999; 99FR-00016273.

XX (VAIS-) INST VAISSEAU & DU SANG.

XX Alemany M, Caen JP, Han ZC;

XX WPI, 2001-488621/53.

XX New elcosa-, tricoso- or pentacosa- to heptacosa-peptides, useful e.g.

XX PT for stimulating hematopoietic stem cell proliferation after chemotherapy

XX PT or radiotherapy or as antiinflammatory agents.

XX PS Example; Page 15; 33pp; French.

XX AAG63418-AA63511 represent peptides which are used in therapy. The

XX CC peptides are haematopoiesis inhibitors, haematopoietic stem cell

XX CC proliferation stimulants, cell differentiation inducers, and chemokine

XX CC antagonists. The peptides are used as a medicament for treating the

XX CC harmful effects of chemotherapy on haematopoietic stem cells; inhibiting

XX CC haematopoietic proliferation, in the treatment of myeloproliferative

XX CC syndromes; cytoprotection against cytotoxic effects, especially in

XX CC protection of haematopoietic cells against apoptosis; medullar expansion

XX CC or purging, in the treatment of medullar insufficiency or medullar grafts

XX CC ; treating inflammation; inhibiting pathological angiogenesis; or

XX CC differentiating abnormal cells into healthy cells. They are also used for

XX CC treatment of essential thrombocytopenia, Vaequez polyglobulia,

XX CC myelofibrosis and chronic leukocytic leukemia. The peptides also show

XX CC some antiviral activity, and are antagonists of chemokines of the CXC

XX CC type and subfamily ELR, especially IL-8, NAP2, groalpha, grobeta and

XX CC grogamma

XX SQ Sequence 23 AA;

Query Match 23.5%; Score 27; DB 4; Length 23;
 Best Local Similarity 33.3%; Pred. No. 6e+03;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 TEDSIKINNGEADAMSL 19
 | : : : : :
 5 TAQLIATLKNQKISLEL 22

Db

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:04:40 ; Search time 39 Seconds

(without alignments)
56.743 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADAMSLOGGF 23Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 228

Minimum DB seq length: 23
Maximum DB seq length: 23Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	24.3	23	2	cytochrome P450 CYP
2	21	18.3	23	2	homeodomain protei
3	20	17.4	23	2	cytic fibrosis tr
4	20	17.4	23	2	mannose-1-phosphat
5	20	17.4	23	2	light-harvesting p
6	19	16.5	23	2	aspartate transami
7	19	16.5	23	2	fibriaral adhesin C
8	19	16.5	23	2	T-cell receptor J-
9	19	16.5	23	2	hypothetical 2.5K
10	19	16.5	23	2	hypothetical prote
11	18.5	16.1	23	2	ribosomal protein
12	18	15.7	23	2	B-1 alpha-amylase
13	18	15.7	23	2	tissue kallikrein
14	18	15.7	23	2	slow muscle tropom
15	18	15.7	23	2	photosystem I 8.0K
16	18	15.7	23	2	93k protein - huma
17	18	15.7	23	2	corticosteroid bin
18	18	15.7	23	2	lysine kinase su
19	18	15.7	23	2	hypothetical prote
20	17	14.8	23	2	lipid transfer pro
21	17	14.8	23	2	cryptidin - mouse (
22	17	14.8	23	2	cryptidin - mouse (
23	17	14.8	23	2	MHC class I histoc
24	17	14.8	23	2	neural cell adhesi
25	17	14.8	23	2	nuclear antigen EB
26	17	14.8	23	2	cysteine proteinas
27	17	14.8	23	2	major fecal allerg
28	17	14.8	23	2	nicotinic acetylch
29	17	14.8	23	2	homeodomain protei

30	17	14.8	23	2	S23518
31	16	13.9	23	2	P00036
32	16	13.9	23	2	D60583
33	16	13.9	23	2	PH1693
34	16	13.9	23	2	S47203
35	16	13.9	23	2	I56028
36	16	13.9	23	2	I50174
37	16	13.9	23	2	D33174
38	16	13.9	23	2	B30968
39	16	13.9	23	2	A48845
40	16	13.9	23	2	D64707
41	16	13.9	23	2	B37843
42	16	13.9	23	2	JH0515
43	15	13.0	23	2	S65379
44	15	13.0	23	2	A29551
45	15	13.0	23	2	PX0011

ALIGNMENTS

RESULT 1

S54339
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S54339
R:Dir, S.; Lake, B.G.; Friedberg, T.; Wolf, C.R.
Biochem. J. 306, 161-166, 1995
A:Title: Expression and alternative splicing of the cytochrome P-450 CYP2A7.
A:Reference number: S54338; MUID:95165049; PMID:7864805
A:Accession: S54339
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-23 <DIN>
A:Cross-references: UNIPARC:UPI000017C0D9

Query Match

Best Local Similarity 24.3%; Score 28; DB 2; Length 23;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 DSIAKIMNGEA 14
DB 6 DSIMKVSQVVA 16

RESULT 2

S60568
homeodomain protein hrox6 - California red abalone (fragment)
C:Species: Haliotis rufescens (California red abalone)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
C:Accession: S60568
R:Deegan, B.M.; Morse, D.E.
Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
A:Title: Identification of eight homeobox-containing transcripts expressed during larval
A:Reference number: S60564; MUID:93372986; PMID:7689904
A:Accession: S60568
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-23 <DEG>
A:Cross-references: UNIPROT:Q25137; UNIPARC:UPI000007984D; EMBL:X79375; NID:g495116; PID
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match

Best Local Similarity 18.3%; Score 21; DB 2; Length 23;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 EADAMSID 20
DB 11 EALAKLD 18

RESULT 3

151922
cyclic fibrosis transmembrane conductance regulator - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C/Accession: 151922
R/McGrath, S.A.; Baau, A.; Zeitlin, P.L.
Am. J. Respir. Cell Mol. Biol. 8, 201-208, 1993
A/Title: Cyclic fibrosis gene and protein expression during fetal lung development.
A/Reference number: 151922; MUID:93152187; PMID:7678968
A/Accession: 151922
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-23 <MCG>
A/Cross-references: UNIPROT:Q23399; UNIPARC:UPI0000087C7C; GB:S54552; NID:g265093; PIDN;
C/Superfamily: cyclic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 17.4%; Score 20; DB 2; Length 23;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDSIAKI 9
DB 3 EDSIASI 9

RESULT 4
A47415
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 37K beta chain - pig (fragment)
N/Alternate names: GDP-mannose pyrophosphorylase 37K beta chain
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C/Accession: A47415
R/Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
J. Biol. Chem. 268, 17943-17950, 1993
A/Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti
A/Reference number: A47415; MUID:93352609; PMID:7688733
A/Contents: liver
A/Accession: A47415
A/Molecule type: protein
A/Residues: 1-23 <SZU>
A/Cross-references: UNIPROT:Q9TRF4; UNIPARC:UPI00000872E8
A/Note: sequence extracted from NCBI backbone (NCBIP:136438)
C/Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C/Function: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A/Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A/Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac
C/Superfamily: mannose-1-phosphate guanylyltransferase
C/Keywords: nucleotidyltransferase

Query Match 17.4%; Score 20; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 16 AMSLDGAF 23
DB 3 ALILVGGY 10

RESULT 5
B54226
light-harvesting protein B-830 alpha-2 chain - Chromatium purpuratum (fragment)
C/Species: Chromatium purpuratum
C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C/Accession: B54226
R/Kerfeld, C.A.; Yeates, T.O.; Thorner, J.P.
Biochemistry 33, 2178-2184, 1994
A/Title: Purification and characterization of the peripheral antenna of the purple-sulfu
A/Reference number: A54226; MUID:94162224; PMID:8117674
A/Accession: B54226
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-23 <KER>
A/Cross-references: UNIPROT:Q7M0J4; UNIPARC:UPI000017CAD4

C/Keywords: antenna complex; light-harvesting polypeptide

Query Match 17.4%; Score 20; DB 2; Length 23;
Best Local Similarity 41.7%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 DSIAKIMGAD 15
DB 9 DKNAKLNHPED 20

RESULT 6
S70780
aspartate transaminase (EC 2.6.1.1) - Xenorhabdus nematophilus (fragment)
N/Alternate names: aspc protein
C/Species: Xenorhabdus nematophilus
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C/Accession: S70780
R/Forst, S.; Maukau, J.; Leisman, G.; Exner, M.; Hancock, R.
Mol. Microbiol. 18, 779-789, 1995
A/Title: Functional and regulatory analysis of the OmpF-like porin, OmpF, of the symbiot
A/Reference number: S70779; MUID:96414477; PMID:8817498
A/Accession: S70780
A/Molecule type: DNA
A/Residues: 1-23 <FOR>
A/Cross-references: UNIPARC:UPI0000175515
A/Experimental source: strain AN6/1
A/Genetics:
A/Gene: aspc
C/Superfamily: aspartate aminotransferase
C/Keywords: aminotransferase

Query Match 16.5%; Score 19; DB 2; Length 23;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 G6ADAMSLD 20
DB 15 GLADSRKAD 23

RESULT 7
A43872
fimbrial adhesin CF29K - Klebsiella pneumoniae (fragment)
C/Species: Klebsiella pneumoniae
C/Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A43872
R/Darfeuille-Michaud, A.; Jallat, C.; Aubel, D.; Siroc, D.; Rich, C.; Siroc, J.; Joly, B
Infect. Immun. 60, 44-55, 1992
A/Title: R-plasmid-encoded adhesive factor in Klebsiella pneumoniae strains responsible f
A/Reference number: A43872; MUID:92104695; PMID:1345909
A/Accession: A43872
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-23 <DAR>
A/Cross-references: UNIPROT:Q9R2G4; UNIPARC:UPI0000083816
A/Experimental source: strain CF504, R plasmid
A/Note: sequence extracted from NCBI backbone (NCBIP:74360)
C/Superfamily: fimbrial adhesin K88

Query Match 16.5%; Score 19; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 6; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 10 MNG-EXADA 16
DB 12 MNGGTRADA 20

RESULT 8
S47194
T-cell receptor J-alpha wNV1.4 - human (fragment)
C/Species: Homo sapiens (man)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C;Accession: S47194
R;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A;Reference number: S40133
A;Accession: S47194
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-23 <PLA>
A;Cross-references: UNIPARC:UPI0000116131; EMBL:X71046; NID:g506578; PIDN:CAA50363.1; PI
C;Keywords: T-cell receptor

Query Match 16.5%; Score 19; DB 2; Length 23;
Best Local Similarity 31.2%; Pred. No. 1.6e+04;
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 7 AKINMGADAMSIDGG 22
Db 1 ASIGTGATSKUTFGTG 16

RESULT 9
JQ0281
hypothetical 2.5K protein (trnR-rps15 intergenic region) - rice chloroplast
C;Species: chloroplast *Oryza sativa* (rice)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JQ0281; S05161
R;Shimada, H.; Whittier, R.F.; Hiratsuka, J.; Maeda, Y.; Hirai, A.; Sugiyra, M.
submitted to JIPID, December 1989
A;Reference number: JQ0200
A;Accession: JQ0281
A;Molecule type: DNA
A;Residues: 1-23 <SHI>
A;Cross-references: UNIPROT:Q37069; UNIPARC:UPI0000095268
R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibaishi, T.; Sakamoto, M.; Mori, M.; Kond
M.; Gen. Genet. 217, 185-194, 1989
A;Title: The complete sequence of the rice (*Oryza sativa*) chloroplast genome: intermolec
of the cereals.
A;Reference number: S05080; MUID:89364698; PMID:2770692
A;Accession: S05161
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-23 <HIR>
A;Cross-references: UNIPARC:UPI0000095268; GB:X15901; NID:g11957; PIDN:CAA33946.1; PID:G
C;Genetics:
A;Note: this sequence was submitted to EMBL, July 1989
C;Keywords: chloroplast
A;Genome: chloroplast

Query Match 16.5%; Score 19; DB 2; Length 23;
Best Local Similarity 46.2%; Pred. No. 1.6e+04;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 10 MNGEADAMSIDGG 22
Db 1 MIGIADVKLNLNG 13

RESULT 10
S58624
hypothetical protein 23 - maize chloroplast
C;Species: chloroplast *Zea mays* (maize)
C;Date: 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: S58624; S58609
R;Maier, R.W.; Neckermann, K.; Igloi, G.L.; Koessel, H.
J. Mol. Biol. 251, 614-628, 1995
A;Title: Complete sequence of the maize chloroplast genome: gene content, hotspots of d
A;Reference number: S58631; MUID:95395841; PMID:7666415
A;Accession: S58624
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-23 <MAI>
A;Cross-references: UNIPROT:Q37069; UNIPARC:UPI0000095268; EMBL:X86563; NID:g902200; PID
A;Genetics: GEN1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A;Accession: S58609
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-23 <MAV>
A;Cross-references: UNIPARC:UPI0000095268; EMBL:X86563; NID:g902200; PIDN:CAA60343.1; PI
A;Genetics: GEN2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics: <GEN1>
A;Map position: IR (A)
A;Genome: chloroplast
C;Genetics: <GEN2>
A;Map position: IR (B)
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 16.5%; Score 19; DB 2; Length 23;
Best Local Similarity 46.2%; Pred. No. 1.6e+04;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 10 MNGEADAMSIDGG 22
Db 1 MIGIADVKLNLNG 13

RESULT 11
S78417
ribosomal protein RL31, mitochondrial [validated] - rat (tentative sequence) (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78417
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78417
A;Molecule type: protein
A;Residues: 1-23 <GOL>
A;Cross-references: UNIPARC:UPI000017C9B5
A;Note: the protein is designated as mitochondrial ribosomal protein L31
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 16.1%; Score 18.5; DB 2; Length 23;
Best Local Similarity 27.3%; Pred. No. 1.9e+04;
Matches 6; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

OY 1 TTESIAKINMGEND-AMSIDG 21
Db 2 STYXSLXDYXKVELALXXDG 23

RESULT 12
I49492
B-1 alpha-amylase - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: I49492
R;Gunnucio, D.L.; Wiebauer, K.; Dranginis, A.; Samuelson, L.C.; Treisman, L.O.; Caldwell,
J. Biol. Chem. 260, 13483-13489, 1985
A;Title: Evolution of the amylase multigene family: YBR/K1 mice express a pancreatic amy
A;Reference number: I49489; MUID:86033801; PMID:2414282
A;Accession: I49492
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-23 <RBS>
A;Cross-references: UNIPARC:UPI00000008D5; GB:M1892; NID:g191914; PIDN:AAA37225.1; PID:
C;Superfamily: alpha-amylase, standard type; alpha-amylase core homology

Query Match 15.7%; Score 18; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 2.3e+04;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 STAKIMNGE 13
 : : |||
 Db 10 TVIRKNGE 18

RESULT 13

S06660
 tissue kallikrein (EC 3.4.21.35) 17K chain, submandibular - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Sep-1993
 C/Accession: S06660
 R/Murakami, K.; Iikagai, H.; Nagumo, N.; Tomita, M.; Shimamura, T.
 FEBS Lett. 257, 400-402, 1989
 A/Title: A cytosolic tissue kallikrein isolated from mouse submandibular glands.
 A/Reference number: S06660; MUID:90060365; PMID:2583286
 A/Accession: S06660
 A/Molecule type: Protein
 A/Residues: 1-23 <MUR>
 A/Cross-references: UNIPARC:UPI0000175BD1
 C/Genetics:
 A/Gene: MGK-6
 C/Superfamily: trypsin; trypsin homology
 C/Keywords: hydrolase; serine proteinase

Query Match 15.7%; Score 18; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 GGF 23
 : : |||
 Db 3 GGF 5

RESULT 14

S66449
 slow muscle tropomyosin - Atlantic salmon (fragment)
 C/Species: Salmo salar (Atlantic salmon)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
 C/Accession: S66449
 R/Healey, D.H.; Bieger, T.; Waddleton, D.M.; Hong, C.; Jackman, D.M.; McGowan, C.; David
 Eur. J. Biochem. 232, 226-234, 1995
 A/Title: Characterisation of fast, slow and cardiac muscle tropomyosins from salmonid fish
 A/Reference number: S66449; MUID:9604805; PMID:7556155
 A/Accession: S66449
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-23 <HEB>
 A/Cross-references: UNIPARC:UPI00001775DE
 C/Superfamily: tropomyosin

Query Match 15.7%; Score 18; DB 2; Length 23;
 Best Local Similarity 30.8%; Pred. No. 2.3e+04;
 Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 EDSIAKIMNGEAD 15
 : : : : |||
 Db 9 ENAINRSMNAEGD 21

RESULT 15

P00690
 photosystem I 8.0K G chain - common tobacco (fragment)
 C/Species: Nicotiana tabacum (common tobacco)
 C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
 C/Accession: P00690
 R/Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
 Plant Physiol. 102, 1259-1267, 1993
 A/Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal are a
 A/Reference number: P00667; MUID:94105345; PMID:8278548
 A/Accession: P00690
 A/Molecule type: protein
 A/Residues: 1-23 <OBO>

A/Cross-references: UNIPARC:UPI00000926B1
 C/Superfamily: photosystem I chain V
 C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 15.7%; Score 18; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 GGF 23
 : : |||
 Db 19 GGF 21

Search completed: June 13, 2006, 02:10:04
 Job time : 41 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:01:14 ; Search time 291 Seconds
(without alignments)
73.111 Million cell updates/sec

Title: US-10-612-162A-2
Perfect score: 1 TTEDSTAKINGEADAMSIDGCF 23
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 segs, 925015592 residues

Total number of hits satisfying chosen parameters: 1271

Minimum DB seq length: 23
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	20.0	23	Q714U0_STRPA	Q714U0 amphora cof
2	22	19.1	23	Q4XJ66_PLACH	Q4XJ66 plasmodium
3	22	19.1	23	Q7RGS8_PLACH	Q7RGS8 plasmodium
4	22	19.1	23	Q9TRK2_CANFA	Q9TRK2 canis famli
5	22	19.1	23	Q9XT63_CANFA	Q9XT63 canis famli
6	22	19.1	23	Q53WU4_MOUSE	Q53WU4 mus musculu
7	22	19.1	23	Q68983_GALPH	Q68983 suid herpes
8	22	19.1	23	Q69391_GALPH	Q69391 suid herpes
9	22	19.1	23	Q9PR80_GADMO	Q9PR80 gadus morhu
10	21	18.3	23	CR43_LITCE	CR43 litorea cae
11	21	18.3	23	G6P1_CANAL	G6P1 candida alb
12	21	18.3	23	Q9HCW9_HUMAN	Q9HCW9 homo sapien
13	21	18.3	23	Q25137_HALRU	Q25137 halicotis ru
14	21	18.3	23	Q4XCL2_PLACH	Q4XCL2 plasmodium
15	21	18.3	23	Q7RMK7_PLACH	Q7RMK7 plasmodium
16	21	18.3	23	Q6UK34_PIG	Q6UK34 sus scrofa
17	21	18.3	23	Q9S8D9_MAIZE	Q9S8D9 zea mays (m
18	21	18.3	23	Q3D4Y1_STRAG	Q3D4Y1 streptococc
19	21	18.3	23	Q86611_SHIVI	Q86611 human immun
20	21	18.3	23	Q99DB8_SHIVI	Q99DB8 human immun
21	20.5	17.8	23	Q9CT79_MOUSE	Q9CT79 mus musculu
22	20	17.4	23	CYC31_DESVU	P81149 desulfovibr
23	20	17.4	23	P83_PSEBP	P83190 pseudis par
24	20	17.4	23	P84_PSEBP	P83191 pseudis par
25	20	17.4	23	Q96W01_FUSOX	Q96W01 fusarium ox
26	20	17.4	23	Q78135_HUMAN	Q78135 homo sapien
27	20	17.4	23	Q78136_HUMAN	Q78136 homo sapien
28	20	17.4	23	Q4YZT8_PLABE	Q4YZT8 plasmodium
29	20	17.4	23	Q29399_RABIT	Q29399 coryctolagus
30	20	17.4	23	Q5EHP9_PIG	Q5EHP9 sus scrofa
31	20	17.4	23	Q9TRF4_PIG	Q9TRF4 sus scrofa

32	20	17.4	23	Q70ZT6_9BRAD	Q70ZT6 bradyrhizob
33	20	17.4	23	Q7M0J4_MARPU	Q7M0J4 marichromat
34	20	17.4	23	Q8KHT3_MYCHO	Q8KHT3 mycoplasma
35	20	17.4	23	Q38XFI_LACSS	Q38XFI lactobacill
36	20	17.4	23	Q08977_MOUSE	Q08977 mus musculu
37	19.5	17.0	23	Q8MG79_CYPCA	Q8MG79 cyprinus ca
38	19	16.5	23	Q3LR94_HUMAN	Q3LR94 homo sapien
39	19	16.5	23	Q5CKR7_HUMAN	Q5CKR7 homo sapien
40	19	16.5	23	Q96EJ6_HUMAN	Q96EJ6 homo sapien
41	19	16.5	23	Q4Y0X6_PLACH	Q4Y0X6 plasmodium
42	19	16.5	23	Q4YLP7_PLABE	Q4YLP7 plasmodium
43	19	16.5	23	Q54AN1_DICTDI	Q54AN1 dictyosteli
44	19	16.5	23	Q8MIP9_SHEEP	Q8MIP9 ovis aries
45	19	16.5	23	Q9GLD1_BOVIN	Q9GLD1 bos taurus

ALIGNMENTS

```

RESULT 1
Q714U0_9STRA PRELIMINARY; PRT; 23 AA.
ID Q714U0_9STRA
AC Q714U0_
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE tmRNA proteolysis tag (Fragment).
GN Name=sstra;
OS Amphora coffaeiformis.
OC plastid.
OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
OC Bacillariophycidae; Thalassiosphaerales; Catenulaceae; Amphora.
OX NCBI_TaxID=59797;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP126;
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Gueneau de Novoa P., Williams K.P.;
RT "The tmRNA website: reductive evolution of tmRNA in plastids and other
endosymbionts.";
RL Nucleic Acids Res. 32:D104-D108(2004).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AF550350; AAQ12666.1; -; Genomic_DNA.
FT NON TR
FT SEQUENCE 23 AA, 2638 MW, D4FA2855C500DEFF CRC64;
Query Match 20.0%; Score 23; DB 2; Length 23;
Best local similarity 55.6%; Pred. No. 5.3e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Q7 6 TAKMNGEA 14
|:|:|:|
Db 8 ISKIIRNNA 16
-----
RESULT 2
Q4XJ66_PLACH PRELIMINARY; PRT; 23 AA.
ID Q4XJ66_PLACH
AC Q4XJ66;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
DE ORFNames=PC400634.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;

```

RA Hall N., Kariya M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafkas F.C., Janse C.J., Barrett B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: CAJ01005496; CAH82968.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2717 MW; 52DE09A26645B3DC CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 44.4%; Pred. No. 7.5e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 DSIAKIMNG 12
Db 1 NSLCKYKNG 9

RESULT 3
Q7RGS8_P1AYO PRELIMINARY; PRT; 23 AA.
AC Q7RGS8;
DT 15-DEC-2003, integrated into UniProtKB/TREMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein (Fragment).
GN ORFNames=PY04268;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perrea M.,
RA Silva J.C., Emolova M.D., Allen J.E., Sengenut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Frazer C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: AABL01001282; EAA16099.1; -; Genomic_DNA.
KM Complete proteome; Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2910 MW; 2A57B5DC8A84F0AA CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;

Best Local Similarity 54.5%; Pred. No. 7.5e+04;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EDSIAKIMNG 13
Db 11 EHSIYIYNG 21

RESULT 4
Q9TRK2_CANFA PRELIMINARY; PRT; 23 AA.
AC Q9TRK2;
DT 01-MAY-2000, integrated into UniProtKB/TREMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Collagen type IV 26 kDa component (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP PROTEIN SEQUENCE.
RA Thoenen P.S., Bauman R., Valli V.E., Mahuran D., Marrano P.M.,
RA Jacobs R.;
RT "Production of anti-NC1 antibody by affected male dogs with X-linked
RT hereditary nephritis: a probe for assessing the NC1 domain of collagen
RT type IV in dogs and humans with hereditary nephritis.";
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: ENSCAFG0000006062; Canis familiaris.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2435 MW; BEA1E30E485953E CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 41.7%; Pred. No. 7.5e+04;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 GEADAMSLDGSF 23
Db 1 GPEPTPSVDHGF 12

RESULT 5
Q9XTE3_CANFA PRELIMINARY; PRT; 23 AA.
AC Q9XTE3;
DT 01-NOV-1999, integrated into UniProtKB/TREMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Adenosine deaminase (Fragment).
GN Name=ADA;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99265967; PubMed=10331940; DOI=10.1006/geno.1999.5772;
RA Li R., Mignot E., Faraco J., Kadotani H., Cantanese J., Zhao B.,
RA Lin X., Hinton L., Ostrander E.A., Patterson D.F., de Jong P.J.;
RT "Construction and characterization of an eightfold redundant dog
RT genomic bacterial artificial chromosome library.";
RL Genomics 58:9-17(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kodatani H., Mignot E.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

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CC -----
DR EMBL; AF103752; AAD40577.1; -; Genomic_DNA.
DR HSSP; P56658; INDM.
DR Ensembl; ENSCAPG00000014519; Canis familiaris.
DR InterPro; IPR006650; A/AMP_deam_AS.
DR PROSITE; PS00485; A_DEAMINASE; UNKNOWN_1.
FT NON TER 1
FT NON TER 23
SQ SEQUENCE 23 AA; 2626 MW; 0C010CEPACF10BE1 CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 23.1%; Pred. No. 7.5e+04;
Matches 3; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 TEDSIKIMGEA 14
DB 2 TEHAVVRLKHDQA 14

RESULT 6
O53WU4 MOUSE PRELIMINARY; PRT; 23 AA.
ID O53WU4;
AC O53WU4;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Gene for alpha 2 (IV) collagen (exon 7) (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8526379; Pubmed=3839908;
RA Kurkinen M., Bernard M.P., Barlow D.P., Chow L.T.;
RT "Characterization of 64-, 123- and 182-base-pair exons in the mouse
RT alpha 2(IV) collagen gene.";
RL Nature 317:177-179(1985).
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CC -----
DR EMBL; X02900; CAE82079.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000031503; Mus musculus.
KM Collagen.
FT NON TER 1
FT NON TER 23
SQ SEQUENCE 23 AA; 2237 MW; AC3F56291DCD2817 CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 7.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 15 DAMSLDGG 22
DB 4 DTVDLPFG 11

RESULT 7
Q68983 9ALPH PRELIMINARY; PRT; 23 AA.
ID Q68983 9ALPH
AC Q68983
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Glycoprotein C precursor (Fragment).
GN Name=GC;
OS Suid herpesvirus 1 (Pseudorabies virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
```

```
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxId=10345;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Becker;
RX MEDLINE=9508163; Pubmed=7989378;
RA Tomiio M., Wilkinson K.S., Ryan P.;
RT "Can a signal sequence become too hydrophobic?";
RL J. Biol. Chem. 269:32016-32021(1994).
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CC -----
DR EMBL; L36970; AAA79967.1; -; Genomic_DNA.
KM Signal.
FT SIGNAL 1
FT NON TER 23
SQ SEQUENCE 23 AA; 2248 MW; B708473E8146D98F CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 62.5%; Pred. No. 7.5e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 MNGEADAM 17
DB 1 MDSLADAM 8

RESULT 8
Q69391 9ALPH PRELIMINARY; PRT; 23 AA.
ID Q69391 9ALPH
AC Q69391;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Glycoprotein C precursor (Fragment).
GN Name=GC;
OS Suid herpesvirus 1 (Pseudorabies virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
NCBI_TaxId=10345;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Becker;
RX MEDLINE=9508163; Pubmed=7989378;
RA Tomiio M., Wilkinson K.S., Ryan P.;
RT "Can a signal sequence become too hydrophobic?";
RL J. Biol. Chem. 269:32016-32021(1994).
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CC -----
DR EMBL; L36969; AAA79966.1; -; Genomic_DNA.
KM Signal.
FT SIGNAL 1
FT NON TER 23
SQ SEQUENCE 23 AA; 2289 MW; B7112B1E8146D98F CRC64;

Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 57.1%; Pred. No. 7.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 DSIAKIM 10
DB 2 DSLARAM 8

RESULT 9
Q9PRS0 GADMO PRELIMINARY; PRT; 23 AA.
ID Q9PRS0 GADMO
AC Q9PRS0;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
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DT 07-FEB-2006, entry version 11.
DE Chymotrypsin isoenzyme CRT2 (Fragment).
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96043258; Pubmed=7584866; DOI=10.1016/0305-0491(95)00094-1;
RA Raaij A.J., Flengsrud R., Sletten K.;
RT "Chymotrypsin isoenzymes in Atlantic cod; differences in kinetics and
RT substrate specificity.";
RL Comp. Biochem. Physiol. 112B:393-398(1995).
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CC -----
FT NON_TER 1 1
FT SEQUENCE 23 AA; 2356 MW; A5EC2A7B73EB3F5E CRC64;
SQ
Query Match 19.1%; Score 22; DB 2; Length 23;
Best Local Similarity 80.0%; Pred. No. 7.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 INNGE 13
Db 14 INNGE 18

RESULT 10
CR43_LITCE STANDARD; PRT; 23 AA.
AC P56244;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Caerin-4.3.
OS Litoria caerulea (Green tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodytidae; Litoria.
OX NCBI_TaxID=30344;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from
RT Litoria caerulea.";
RL J. Chem. Res. 198:910-936(1993).
CC -1- FUNCTION: Antibacterial peptide, that adopts an alpha helical
CC conformation which can disrupt bacterial membranes. Each caerin
CC displays a different antimicrobial specificity.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC glands.
CC -1- MASS SPECTROMETRY: MW=2353; METHOD=PAB; RANGE=1-23; NOTE=Ref.1.
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CC -----
KW Amidation; Amphibian defense peptide; Antibiotic; Antimicrobial;
KW Direct protein sequencing.
FT PEPTIDE 1 23
FT MOD_RES 23 23
FT SEQUENCE 23 AA; 2356 MW; B98FDB08B6ADC9D CRC64;
SQ
Query Match 18.3%; Score 21; DB 1; Length 23;
Best Local Similarity 45.5%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 8 KINNGEADAMS 18
Db 5 KIRKAGADLAS 15

RESULT 11
G6PI_CANAL STANDARD; PRT; 23 AA.
ID G6PI_CANAL
AC P83780;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, entry version 1.
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Fragments).
GN Name=GPII;
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND ANTIGENICITY.
RC STRAIN=SC5314; TISSUE=Protoclast;
RX Pubmed=15378761; DOI=10.1002/pmic.200400903;
RA Pitarach A., Abian J., Carrascal M., Sanchez M., Nombela C., Gil C.;
RT "Proteomics-based identification of novel Candida albicans antigens
RT for diagnosis of systemic candidiasis in patients with underlying
RT hematological malignancies.";
RL Proteomics 4:3084-3106(2004).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -1- PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-
CC phosphate and glycerone phosphate from D-glucose: step 2.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasm.
CC -1- MISCELLANEOUS: Has antigenic properties. Elicits a specific immune
CC response in systemic candidiasis human patients undergoing
CC malignant hematological disorders.
CC -1- SIMILARITY: Belongs to the GPI family.
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CC -----
DR InterPro: IPR001672; G6P_Isoomerase.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; PARTIAL.
DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; PARTIAL.
KW Antigen; Direct protein sequencing; Glucogenesis; Glycolysis;
KW Isomerase.
FT CHAIN <1 >23
FT FT Glucose-6-phosphate isomerase.
FT NON_CONS 12 13
FT NON_TER 1 1
FT SEQUENCE 23 AA; 2590 MW; 8A17665F26D8BF35 CRC64;
SQ
Query Match 18.3%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTED 4
Db 8 TTED 11

RESULT 12
Q9HCW9_HUMAN PRELIMINARY; PRT; 23 AA.
ID Q9HCW9_HUMAN
AC Q9HCW9;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Orlovsky I.V., Sverdlowa P.S., Rubtsov P.M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AJ295613; CAC06615.1; -, Genomic_DNA.
DR PIR: A41814; A41814; Homo sapiens.
DR Ensembl: ENSG00000112964; Homo sapiens.
DR GO: GO:0004872; F:receptor activity; IEA.
KM Receptor.
FT NON_TER
SQ SEQUENCE 23 AA; 2426 MW; 9AD833A0F1DD699E CRC64;

Query Match 18.3%; Score 21; DB 2; Length 23;
Best Local Similarity 57.1%; Pred. No. 1.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 G6ADAMS 18
DB 14 GSSDAFS 20

RESULT 13
ID Q25137 HALRU PRELIMINARY; PRT; 23 AA.
AC Q25137;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Hrox6 protein (Fragment).
GN Name=hrox6;
OS Halictus rufescens (California red abalone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Halictoidae; Halictidae; Halictis.
OX NCBI_TaxID=6454;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=93372986; PubMed=7689904;
RA Degnan B.M., Morse D.E.;
RT "Identification of eight homeobox-containing transcripts expressed
RT during larval development and at metamorphosis in the gastropod
RT mollusc Halictis rufescens.";
RL Mol. Mar. Biol. Biotechnol. 2:1-9(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Degnan B.M.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: X79375; CAA55920.1; -, mRNA.
DR PIR: S60568; S60568.
DR GO: GO:0005634; C:nucleus; IEA.
KM Nuclear protein.
FT NON_TER
SQ SEQUENCE 23 AA; 2689 MW; 56D81AE184E2843D CRC64;

Query Match 18.3%; Score 21; DB 2; Length 23;
Best Local Similarity 62.5%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 EADAMSLD 20
DB 11 EALAKLKD 18

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RESULT 14
ID Q4XCL2 PLACH PRELIMINARY; PRT; 23 AA.
AC Q4XCL2;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC403366.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5625;
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.M.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. II,
RA Kafatos F.C., Jense C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: CAJ01007562; CAH85360.1; -, Genomic_DNA.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 23 AA; 2830 MW; FB1EAB0897A6D2CB CRC64;

Query Match 18.3%; Score 21; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 DAMSLD 20
DB 18 DALCLD 23

RESULT 15
ID Q7RMK7 PLAYO PRELIMINARY; PRT; 23 AA.
AC Q7RMK7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein (Fragment).
GN ORFNames=PY02172;
DS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selenkoff J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallen S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedeghan M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. II, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

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RA  Garucci D.J. :
RT  "Genome sequence and comparative analysis of the model rodent malaria
RL  parasite Plasmodium yoelii yoelii.",
RL  Nature 419:512-519(2002) .
CC  -!- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
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CC  -----
DR  EMBL; AABL01000596; EAA21602.1; -!- Genomic DNA.
KM  Complete proteome; Hypothetical protein.
FT  NON_TER      1
SQ  SEQUENCE      23 AA;  2856 MW;  D39AB39D98B96070 CRC64;

Query Match      18.3%; Score 21; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 KINNGE 13
      ||||:
Db      12 KINNGQ 17
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Search completed: June 13, 2006, 02:09:20
Job time : 294 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:09:35 ; Search time 49 Seconds
(without alignments)
41.086 Million cell updates/sec

Title: US-10-612-162A-2
Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADAMSLDGF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 4481

Minimum DB seq length: 23
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pdp:*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pdp:*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pdp:*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pdp:*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCTUS.COMB.pdp:*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE.COMB.pdp:*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfill1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	28.7	23	1	US-08-568-147B-14 Sequence 14, Appl
2	28	24.3	23	1	US-08-178-477B-17 Sequence 17, Appl
3	27	23.5	23	2	US-08-860-808E-25 Sequence 25, Appl
4	26	22.6	23	1	US-07-936-163-41 Sequence 41, Appl
5	25	21.7	23	1	US-08-093-383-23 Sequence 23, Appl
6	25	21.7	23	1	US-08-093-383-27 Sequence 27, Appl
7	24	20.9	23	1	US-08-808-550-26 Sequence 26, Appl
8	24	20.9	23	2	US-09-128-450-7 Sequence 7, Appl
9	24	20.9	23	2	US-09-220-731-18 Sequence 18, Appl
10	24	20.9	23	2	US-09-823-494-7 Sequence 7, Appl
11	24	20.9	23	2	US-08-981-527A-17 Sequence 17, Appl
12	24	20.9	23	2	US-10-147-936B-17 Sequence 17, Appl
13	24	20.9	23	2	US-09-270-767-60291 Sequence 60291, A
14	24	20.9	23	2	US-09-559-021-3 Sequence 3, Appl
15	24	20.9	23	3	US-10-071-214-5 Sequence 5, Appl
16	23	20.0	23	1	US-08-112-208C-13 Sequence 13, Appl
17	23	20.0	23	1	US-08-248-819A-15 Sequence 15, Appl
18	23	20.0	23	1	US-08-337-646A-33 Sequence 33, Appl
19	23	20.0	23	1	US-08-856-531-13 Sequence 13, Appl
20	23	20.0	23	1	US-08-856-034-13 Sequence 13, Appl
21	23	20.0	23	1	US-08-667-809B-4 Sequence 4, Appl
22	23	20.0	23	1	US-08-927-326-33 Sequence 33, Appl
23	23	20.0	23	2	US-09-001-984C-52 Sequence 52, Appl
24	23	20.0	23	2	US-08-981-527A-19 Sequence 19, Appl
25	23	20.0	23	2	US-09-379-820A-13 Sequence 13, Appl
26	23	20.0	23	2	US-09-396-347F-52 Sequence 52, Appl

27	23	20.0	23	2	US-09-502-829-1 Sequence 1, Appl
28	23	20.0	23	2	US-10-147-936B-19 Sequence 19, Appl
29	23	20.0	23	2	US-09-270-767-38586 Sequence 38586, A
30	23	20.0	23	2	US-09-270-767-53803 Sequence 53803, A
31	23	20.0	23	2	US-09-270-767-58329 Sequence 58329, A
32	23	20.0	23	2	US-09-820-053A-146 Sequence 146, App
33	23	20.0	23	3	US-10-071-026-54 Sequence 54, Appl
34	23	20.0	23	3	US-10-071-214-4 Sequence 4, Appl
35	23	20.0	23	7	5221732-3 Patent No. 5221732
36	23	20.0	23	7	5254535-24 Patent No. 5254535
37	23	20.0	23	7	5254535-24 Patent No. 5254535
38	22.5	19.6	23	1	US-08-460-890A-54 Sequence 54, Appl
39	22.5	19.6	23	2	US-08-167-641C-54 Sequence 54, Appl
40	22.5	19.6	23	2	US-08-460-971A-54 Sequence 54, Appl
41	22.5	19.6	23	2	US-08-462-040-54 Sequence 54, Appl
42	22	19.1	23	1	US-08-466-953A-44 Sequence 44, Appl
43	22	19.1	23	2	US-08-341-018-34 Sequence 34, Appl
44	22	19.1	23	2	US-08-470-335-215 Sequence 215, App
45	22	19.1	23	2	US-08-470-339-215 Sequence 215, App

ALIGNMENTS

RESULT 1
US-08-568-147B-14
Sequence 14, Application US/08568147B
Patent No. 5783422
GENERAL INFORMATION:
APPLICANT: Sumitani, Yoshinori
APPLICANT: Kato, Hiroshi
APPLICANT: Sekiguchi, Kiyoshi
APPLICANT: Takeda, Katsunichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL
TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568.147B
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 800,952
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8425
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-568-147B-14
Query Match 28.7%; Score 33; DB 1; Length 23;
Best Local Similarity 46.2%; Pred. No. 1e+02;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 9 INNGADAMSIDG 21

Db 5 IFNGDADLSGMTG 17

RESULT 2

US-08-178-477B-17

; Sequence 17, Application US/08178477B

; Patent No. 5756343

; GENERAL INFORMATION:

; APPLICANT: MU, CARL; CLOS, JOACHIM;

; APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR

; TITLE OF INVENTION: CELL STRESS

; TRANSCRIPTIONAL FACTORS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/178,477B

; FILING DATE: 07-JAN-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/617,910

; FILING DATE: 26-NOV-1990

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4103US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; TELETYPE: 421792

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-178-477B-17

Query Match 24.3%; Score 28; DB 1; Length 23;

Best Local Similarity 43.8%; Pred. No. 7e+02; Mismatches 5; Indels 2; Gaps 1;

Matches 7; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KINNGADAMSIDG 23

Db 5 KVMRGROD-NLDSRF 18

RESULT 3

US-08-860-808B-25

; Sequence 25, Application US/08860808E

; Patent No. 6207399

; GENERAL INFORMATION:

; APPLICANT: HEMKER, HENDRIK C

; APPLICANT: RUIKERS, DIRK T

; APPLICANT: TESSER, GODEFRIDUS I

; TITLE OF INVENTION: METHODS OF DETERMINING ENDOGENOUS THROMBIN POTENTIAL

; TITLE OF INVENTION: (exp) AND THROMBIN SUBSTRATES FOR USE IN SAID METHODS

; FILE REFERENCE: HEMKER

; CURRENT APPLICATION NUMBER: US/08/860,808E

; CURRENT FILING DATE: 1997-09-05

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 25

; LENGTH: 23

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:peptide

; US-08-860-808B-25

Query Match 23.5%; Score 27; DB 2; Length 23;

Best Local Similarity 41.7%; Pred. No. 1e+03; Mismatches 4; Indels 0; Gaps 0;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 11 NGEADAMSIDG 22

Db 3 SGEGDPLAEGG 14

RESULT 4

US-07-936-163-41

; Sequence 41, Application US/07936163

; Patent No. 5743477

; GENERAL INFORMATION:

; APPLICANT: WALSH, TERENCE A

; APPLICANT: MERLO, DONALD J

; APPLICANT: HOUTCHENS, ROBERT A

; APPLICANT: STRICKLAND, JAMES A

; APPLICANT: ORR, GREGORY L

; TITLE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR

; TITLE OF INVENTION: PLANT PROTECTION

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THOMAS D. ZINDRICK

; STREET: 9002 PURDUE ROAD

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: US

; ZIP: 46268-1189

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/936,163

; FILING DATE: 27-AUG-1992

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: ZINDRICK, THOMAS D

; REGISTRATION NUMBER: 32,185

; REFERENCE/DOCKET NUMBER: C-38,424A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-1869

; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-07-936-163-41

Query Match 22.6%; Score 26; DB 1; Length 23;

Best Local Similarity 66.7%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 17 MSIDG 22

Db 9 LSIDG 14

```
RESULT 5
US-08-093-383-23
; Sequence 23, Application US/08093383
; Patent No. 5489529
; GENERAL INFORMATION:
; APPLICANT: DeBoer, Herman A.
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,383
; FILING DATE: 14-JUL-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07/619827
; FILING DATE: 28-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/198824
; FILING DATE: 05-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/632361
; FILING DATE: 19-JUL-1984
; INFORMATION FOR SEQ ID NO: 23:
; APPLICATION NUMBER: 06/303687
; FILING DATE: 18-SEP-1981
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: P35,910
; REFERENCE/DOCKET NUMBER: 46C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-093-383-23

Query Match      21.7%; Score 25; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      16 AMSLDGCF 23
Db      4 AMSLSGLF 11

RESULT 6
US-08-093-383-27
; Sequence 27, Application US/08093383
; Patent No. 5489529
; GENERAL INFORMATION:
; APPLICANT: DeBoer, Herman A.
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
```

```
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,383
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 07/619827
FILING DATE: 28-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/632361
FILING DATE: 19-JUL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/303687
FILING DATE: 18-SEP-1981
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 46C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-093-383-27

Query Match      21.7%; Score 25; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      16 AMSLDGCF 23
Db      4 AMSLSGLF 11

RESULT 7
US-08-808-550-26
; Sequence 26, Application US/08080550
; Patent No. 5871992
; GENERAL INFORMATION:
; APPLICANT: Teboer, George W.
; APPLICANT: Hilbert, Timothy P.
; TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,550
; FILING DATE: 26-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-001 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: bovine
;
US-08-808-550-26
```

```
Query Match 20.9%; Score 24; DB 1; Length 23;
Best Local Similarity 31.8%; Pred. No. 3.2e+03;
Matches 7; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```
OY 2 TEDSIKINNGEADMSLDGCF 23
Db 2 TVDSILQTDSTLIGALIVPGF 23
```

```
RESULT 8
US-09-128-450-7
; Sequence 7, Application US/09128450
; Patent No. 6211149
; GENERAL INFORMATION:
; APPLICANT: Chesebro, Bruce W
; APPLICANT: Chaghey, Byron W
; APPLICANT: Chabry, Joelle
; APPLICANT: Priola, Sueette
; TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
; FILE REFERENCE: 50121
; CURRENT APPLICATION NUMBER: US/09/128,450
; CURRENT FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Hamster sp.
;
US-09-128-450-7
```

```
Query Match 20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 46.7%; Pred. No. 3.2e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 8 KINNGEADMSLDG 22
Db 5 KHMAGAAAGAVVG 19
```

```
RESULT 9
US-09-220-731-18
; Sequence 18, Application US/09220731A
; Patent No. 6232088
; GENERAL INFORMATION:
; APPLICANT: Phatrien Medical, Inc.
```

```
; APPLICANT: Richard L. Franklin
; APPLICANT: Yves St. Pierre
; TITLE OF INVENTION: Treatment and Prevention of Immune
; FILE REFERENCE: 314572-101D
; CURRENT APPLICATION NUMBER: US/09/220,731A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: PCT/SE93/00455
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 08/338,501
; EARLIER FILING DATE: 1994-11-22
; EARLIER APPLICATION NUMBER: 08/385,540
; EARLIER FILING DATE: 1995-02-08
; EARLIER APPLICATION NUMBER: 08/486,820
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/600,273
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Atlantic cod
;
US-09-220-731-18
```

```
Query Match 20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 30.8%; Pred. No. 3.2e+03;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 11 NGEADMSLDGCF 23
Db 10 HSGAHQVSLNSGY 22
```

```
RESULT 10
US-09-823-494-7
; Sequence 7, Application US/09823494
; Patent No. 6355610
; GENERAL INFORMATION:
; APPLICANT: Chesebro, Bruce W
; APPLICANT: Chaghey, Byron W
; APPLICANT: Chabry, Joelle
; APPLICANT: Priola, Sueette
; TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
; FILE REFERENCE: 50121
; CURRENT APPLICATION NUMBER: US/09/823,494
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/128,450
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Hamster sp.
;
US-09-823-494-7
```

```
Query Match 20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 46.7%; Pred. No. 3.2e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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```
OY 8 KINNGEADMSLDG 22
Db 5 KHMAGAAAGAVVG 19
```

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RESULT 11
US-08-981-527A-17
; Sequence 17, Application US/08981527A
; Patent No. 6410262
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
```

```
; APPLICANT: Kerkman, Richard
; APPLICANT: Broekhuizen, Cornelis P.
; TITLE OF INVENTION: No. 6410262el Secretion Factors for
; TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methods
; FILE REFERENCE: GCX322-US
; CURRENT APPLICATION NUMBER: US/08/981,527A
; CURRENT FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: PCT/NL96/00278
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Sulfolobus solfataricus
; US-08-981-527A-17

Query Match      20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      5 SIAKIM 11
      :||||:|
Db      3 TIAKVN 9

RESULT 12
; US-10-147-936B-17
; Sequence 17, Application US/10147936B
; Patent No. 6692951
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; APPLICANT: Kerkman, Richard
; APPLICANT: Broekhuizen, Cornelis P.
; TITLE OF INVENTION: No. 6692951el Secretion Factors for
; TITLE OF INVENTION: Gram-Positive Microorganisms Genes Encoding Them and Methods
; FILE REFERENCE: GCX322-US
; CURRENT APPLICATION NUMBER: US/10/147,936B
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US/08/981,527
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: PCT/NL96/00278
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Sulfolobus solfataricus
; US-10-147-936B-17

Query Match      20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      5 SIAKIM 11
      :||||:|
Db      3 TIAKVN 9

RESULT 13
; US-09-270-767-60291
; Sequence 60291, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60291
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-60291

Query Match      20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 41.7%; Pred. No. 3.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      12 GEADAMSLDGGF 23
      :|||:|
Db      6 GEARPPYANGTF 17

RESULT 14
; US-09-559-021-3
; Sequence 3, Application US/09559021
; Patent No. 6872519
; GENERAL INFORMATION:
; APPLICANT: WOLFE, JON
; APPLICANT: SOKOLOFF, ALEXANDER
; TITLE OF INVENTION: PROCESS FOR UTILIZING EPITOPES RECOGNIZED BY NATURAL ANTIBODIES
; FILE REFERENCE: MIRUS.014.02
; CURRENT APPLICATION NUMBER: US/09/559,021
; CURRENT FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Bacteriophage T7
; US-09-559-021-3

Query Match      20.9%; Score 24; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 3.2e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      9 IMNGEADAMSID 20
      :|:|:|
Db      5 VMLGDPNSSVD 16

RESULT 15
; US-10-071-214-5
; Sequence 5, Application US/10071214
; Patent No. 7019194
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON-3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Sus scrofa
; US-10-071-214-5

Query Match      20.9%; Score 24; DB 3; Length 23;
Best Local Similarity 37.5%; Pred. No. 3.2e+03;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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Qy	7	AKIMGEADAMSLDGG	22
Db	1	AGIPNSKTNACNGDSG	16

Search completed: June 13, 2006, 02:10:59
Job time : 51 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 02:21:20 ; Search time 179 Seconds
(without alignments)
59.519 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSIKIMNGEADAMSIDGCF 23

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Gapop 10.0 , Gapext 0.5

Searched:

2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 23

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	115	100.0	23	4	US-10-612-162-2
2	30	26.1	23	5	US-10-862-195-357
3	27	23.5	23	4	US-10-422-536-91
4	27	23.5	23	5	US-10-484-568-63
5	27	23.5	23	5	US-10-504-905-69
6	27	23.5	23	5	US-10-510-246-23
7	27	23.5	23	6	US-11-069-642-91
8	26	22.6	23	3	US-09-734-417-5
9	26	22.6	23	4	US-10-105-232-375
10	26	22.6	23	4	US-10-189-437-362
11	26	22.6	23	5	US-10-860-050-375
12	25	21.7	23	4	US-10-174-410-91
13	25	21.7	23	4	US-10-400-083-10
14	24	20.9	23	3	US-09-823-494-7
15	24	20.9	23	4	US-10-071-214-5
16	24	20.9	23	4	US-10-147-936-17
17	24	20.9	23	4	US-10-029-386-32425
18	24	20.9	23	4	US-10-169-103-6
19	24	20.9	23	5	US-10-795-676-60
20	24	20.9	23	5	US-10-928-626-54
21	24	20.9	23	5	US-10-450-763-32638
22	24	20.9	23	5	US-10-509-180-2
23	24	20.0	23	3	US-09-820-053A-146
24	23	20.0	23	3	US-09-974-026-54
25	23	20.0	23	4	US-10-097-065-447
26	23	20.0	23	4	US-10-071-214-4
27	23	20.0	23	4	US-10-147-936-19

28	23	20.0	23	4	US-10-277-693A-13	Sequence 13, Appl
29	23	20.0	23	4	US-10-109-171-146	Sequence 146, App
30	23	20.0	23	4	US-10-083-259-158	Sequence 158, App
31	23	20.0	23	4	US-10-231-417-445	Sequence 445, App
32	23	20.0	23	4	US-10-109-274A-158	Sequence 158, App
33	23	20.0	23	4	US-10-372-876-447	Sequence 447, App
34	23	20.0	23	4	US-10-240-641-26	Sequence 26, Appl
35	23	20.0	23	5	US-10-839-525-146	Sequence 146, App
36	23	20.0	23	6	US-11-136-186-146	Sequence 146, App
37	23	20.0	23	6	US-11-111-953-519	Sequence 519, App
38	22	19.1	23	3	US-09-971-980-35	Sequence 35, Appl
39	22	19.1	23	4	US-10-174-410-93	Sequence 93, Appl
40	22	19.1	23	4	US-10-352-786-1881	Sequence 1881, Ap
41	22	19.1	23	4	US-10-352-786-1886	Sequence 1886, Ap
42	22	19.1	23	4	US-10-352-786-1894	Sequence 1894, Ap
43	22	19.1	23	4	US-10-352-786-1902	Sequence 1902, Ap
44	22	19.1	23	4	US-10-377-714-25	Sequence 25, Appl
45	22	19.1	23	4	US-10-372-473-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-10-612-162-2
; Sequence 2, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-2

Query Match      100.0%; Score 115; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6,2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTEDSIKIMNGEADAMSIDGCF 23
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DB      1 TTEDSIKIMNGEADAMSIDGCF 23

RESULT 2
US-10-862-195-357
; Sequence 357, Application US/10862195
; Publication No. US20050164324A1
; GENERAL INFORMATION:
; APPLICANT: GYGI, STEVEN P.
; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
; FILE REFERENCE: 58890(70207)
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/476,010
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 2245
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
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FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-357

Query Match 26.1%; Score 30; DB 5; Length 23;
Best Local Similarity 54.5%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 GEADAMSIDCG 22
DB 3 GEGEASADCG 13

RESULT 3
US-10-422-536-91
Sequence 91, Application US/10422536
Publication No. US20040014100A1
GENERAL INFORMATION:
APPLICANT: Kinsella, Todd
APPLICANT: Lorens, James
APPLICANT: Pray, Todd
APPLICANT: Bennett, Mark
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: A-71433-1/AMP/CYO
CURRENT APPLICATION NUMBER: US/10/422,536
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US 60/187,130
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 09/800,770
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: US 10/232,758
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 168
SOFTWARE: PatentIn version 3.2
SEQ ID NO 91
LENGTH: 23
TYPE: PRT
ORGANISM: Synechocystis PCC6803
US-10-422-536-91

Query Match 23.5%; Score 27; DB 4; Length 23;
Best Local Similarity 31.6%; Pred. No. 5e+03;
Matches 6; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTEDSIKINNGEADAMSL 19
DB 4 STQSALSKDPENKRDHVL 22

RESULT 4
US-10-484-568-63
Sequence 63, Application US/10484568
Publication No. US20040248194A1
GENERAL INFORMATION:
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Lewis, Claire
APPLICANT: Robinson, Jeffrey
TITLE OF INVENTION: Peptide Screen
FILE REFERENCE: 4-32520/32360/361
CURRENT APPLICATION NUMBER: US/10/484,568
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 23
TYPE: PRT
ORGANISM: Homo sapiens
US-10-484-568-63

Query Match 23.5%; Score 27; DB 5; Length 23;
Best Local Similarity 41.7%; Pred. No. 5e+03;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 NGEADAMSLDGC 22
DB 2 SGECDPLAEGCG 13

RESULT 5
US-10-504-905-69
Sequence 69, Application US/10504905
Publication No. US20050118598A1
GENERAL INFORMATION:
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Lewis, Claire
APPLICANT: Robinson, Jeffrey
TITLE OF INVENTION: ORGANIC COMPOUNDS
FILE REFERENCE: DC/4-32360A/32361
CURRENT APPLICATION NUMBER: US/10/504,905
CURRENT FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: PCT/EP03/01698
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: GB 0203882.6
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: GB 0203883.4
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: GB 0217067.8
PRIOR FILING DATE: 2002-07-23
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 23
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(23)
OTHER INFORMATION: anti-angiogenic peptide
US-10-504-905-69

Query Match 23.5%; Score 27; DB 5; Length 23;
Best Local Similarity 41.7%; Pred. No. 5e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 NGEADAMSLDGC 22
DB 2 SGECDPLAEGCG 13

RESULT 6
US-10-510-246-23
Sequence 23, Application US/10510246
Publication No. US20060040334A1
GENERAL INFORMATION:
APPLICANT: Xzillion GmbH & Co. KG
APPLICANT: Thompson, Andrew H.
APPLICANT: Hamon, Christian
APPLICANT: Kuhn, Karsten
APPLICANT: Weyer, Markus
APPLICANT: Schaefer, Juergen
APPLICANT: Neumann, Thomas
TITLE OF INVENTION: Method For Characterising Analytes
FILE REFERENCE: 01073/0201939-US0
CURRENT APPLICATION NUMBER: US/10/510,246
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: PCT/GB03/01485
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 02252440.9
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 23
TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:labelled
; OTHER INFORMATION: peptide
; US-10-510-246-23
Query Match      23.5%; Score 27; DB 5; Length 23;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 TEDSIKIMN 11
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Db      5 TEDYSLILN 14

RESULT 7
US-11-069-642-91
; Sequence 91, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: PRAY, TODD R.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-91
Query Match      23.5%; Score 27; DB 6; Length 23;
Best Local Similarity 31.6%; Pred. No. 5e+03;
Matches 6; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 TTEDSIKIMNGEADANSL 19
      |||::||
Db      4 STQSALSKDPEKRDHML 22

RESULT 8
US-09-734-417-5
; Sequence 5, Application US/09734417
; Patent No. US20020081312A1
; GENERAL INFORMATION:
; APPLICANT: Priest, Jeffrey W.
; APPLICANT: Lammie, Patrick J.
; APPLICANT: Kwon, James P.
; APPLICANT: Arrowood, Michael J.
; APPLICANT: Moss, Dolynn M.
; TITLE OF INVENTION: RECOMBINANT CRYPTOSPORIDIUM PARVUM
; TITLE OF INVENTION: ANTIGEN AND DETECTION OF ANTIBODIES THEREO
; FILE REFERENCE: 14114,035703
; CURRENT APPLICATION NUMBER: US/09/734,417
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: 60/169,797
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/114,054
; PRIOR FILING DATE: 1999-12-30
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = g or s
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-09-734-417-5
Query Match      22.6%; Score 26; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 SLDGG 22
      |||||
Db      17 SLDGG 21

RESULT 9
US-10-105-232-375
; Sequence 375, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGACH, SAMUEL.
; APPLICANT: BOGACH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 375
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-375
Query Match      22.6%; Score 26; DB 4; Length 23;
Best Local Similarity 33.3%; Pred. No. 7.1e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 TTEDSIKIMNGEAD 15
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Db      5 TTIDDEVVELKDVED 19

RESULT 10
US-10-189-437-362
; Sequence 362, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGACH, SAMUEL.
; APPLICANT: BOGACH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; PRIOR FILING DATE: 2002-07-08
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;; PRIOR APPLICATION NUMBER: 10/105,232
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: 09/984,057
;; PRIOR FILING DATE: 2001-10-26
;; PRIOR APPLICATION NUMBER: 60/303,396
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: 60/278,761
;; PRIOR FILING DATE: 2001-03-27
;; NUMBER OF SEQ ID NOS: 729
;; SOFTWARE: PatentIn 2.1
;; SEQ ID NO 362
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Plasmodium falciparum
US-10-189-437-362

Query Match 22.6%; Score 26; DB 4; Length 23;
Best Local Similarity 33.3%; Pred. No. 7.1e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEAD 15
|||:|:|
Db 5 TTIDEVELKDVED 19

RESULT 11
US-10-860-050-375
; Sequence 375, Application US/10860050
; Publication No. US20050202415A1
; GENERAL INFORMATION:
; APPLICANT: BOGACH, SAMUEL
; TITLE OF INVENTION: REPILKIN PEPTIDES AND USES THEREOF
; FILE REFERENCE: 09425/469071
; CURRENT APPLICATION NUMBER: US/10/860,050
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/531,686
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 60/504,958
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/476,186
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 375
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-860-050-375

Query Match 22.6%; Score 26; DB 5; Length 23;
Best Local Similarity 33.3%; Pred. No. 7.1e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEAD 15
|||:|:|
Db 5 TTIDEVELKDVED 19

RESULT 12
US-10-174-410-91
; Sequence 91, Application US/10174410
; Publication No. US20030073134A1
; GENERAL INFORMATION:
; APPLICANT: Louie, Gordon V.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
; TITLE OF INVENTION: 2C-METHYL-D-ERYTHRITOL, 2,4-CYCLODIPHOSPHATE SYNTHASE MECPs
; FILE REFERENCE: 52498200300
; CURRENT APPLICATION NUMBER: US/10/174,410
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/299,058

;; PRIOR FILING DATE: 2001-06-18
;; NUMBER OF SEQ ID NOS: 336
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 91
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: B. melitensis
US-10-174-410-91

Query Match 21.7%; Score 25; DB 4; Length 23;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 MNGEADA 16
:|:|
Db 16 LNGTHSDA 22

RESULT 13
US-10-400-083-10
; Sequence 10, Application US/10400083
; Publication No. US20040186056A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Portka, Kimmo
; APPLICANT: Christen, Sven
; TITLE OF INVENTION: HMG2 Peptides and Related Molecules
; TITLE OF INVENTION: that Selectively Home to Tumor Blood Vessels and Tumor Cells
; FILE REFERENCE: P-LJ 5662
; CURRENT APPLICATION NUMBER: US/10/400,083
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 10/116,866
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-083-10

Query Match 21.7%; Score 25; DB 4; Length 23;
Best Local Similarity 38.5%; Pred. No. 1e+04;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 DSIAKIMNGEADA 16
:|:|:|
Db 2 EKVPGKGGKADA 14

RESULT 14
US-09-823-494-7
; Sequence 7, Application US/09823494
; Publication No. US20010041790A1
; GENERAL INFORMATION:
; APPLICANT: Chesebro, Bruce W
; APPLICANT: Caughey, Byron W
; APPLICANT: Chabry, Joelle
; APPLICANT: Priola, Suseete
; TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
; FILE REFERENCE: 50121
; CURRENT APPLICATION NUMBER: US/09/823,494
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/128,450
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Hamster sp.
US-09-823-494-7

Query Match 20.9%; Score 24; DB 3; Length 23;
Best Local Similarity 46.7%; Pred. No. 1.5e+04;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 8 KINNGEADAMSLDGG 22
DB 5 KHMAGAAAGAVVGG 19

RESULT 15

US-10-071-214-5
; Sequence 5, Application US/10071214
; Publication No. US2003006099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON-3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-071-214-5

Query Match 20.9%; Score 24; DB 4; Length 23;
Best Local Similarity 37.5%; Pred. No. 1.5e+04;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 7 AKINNGEADAMSLDGG 22
DB 1 AGIPNSKTNACNGDSG 16

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Title: US-10-612-162A-2
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Searched: 64916 segs, 12643201 residues

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SUMMARIES

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4	19	16.5	23	US-10-787-734-136	Sequence 136, App1
5	18	16.5	23	US-10-787-734-139	Sequence 139, App1
6	18	15.7	23	US-11-252-276-124	Sequence 124, App1
7	18	15.7	23	US-11-122-986-457	Sequence 457, App1
8	17	14.8	23	US-09-731-899-21	Sequence 21, App1
9	17	14.8	23	US-10-490-949-36	Sequence 36, App1
10	17	14.8	23	US-11-251-465-53	Sequence 53, App1
11	17	14.8	23	US-11-169-140-26	Sequence 26, App1
12	16	13.9	23	US-09-949-925-291	Sequence 291, App1
13	16	13.9	23	US-10-515-429-30	Sequence 30, App1
14	16	13.9	23	US-11-219-563-41	Sequence 41, App1
15	16	13.9	23	US-11-259-950-21	Sequence 21, App1
16	16	13.9	23	US-11-334-622-21	Sequence 21, App1
17	16	13.9	23	US-11-038-753-20	Sequence 20, App1
18	15	13.0	23	US-10-514-462-9	Sequence 9, App1
19	15	13.0	23	US-10-787-734-140	Sequence 140, App1
20	15	13.0	23	US-11-251-465-51	Sequence 51, App1
21	15	13.0	23	US-11-251-465-72	Sequence 72, App1
22	15	13.0	23	US-11-251-465-103	Sequence 103, App1
23	15	13.0	23	US-11-223-738-27	Sequence 27, App1
24	15	13.0	23	US-11-122-986-439	Sequence 439, App1
25	15	13.0	23	US-11-268-690-6	Sequence 6, App1

26	14	12.2	23	1	US-09-949-925-242	Sequence 242, App1
27	14	12.2	23	1	US-09-949-925-295	Sequence 295, App1
28	14	12.2	23	6	US-10-706-435A-12	Sequence 12, App1
29	14	12.2	23	6	US-10-706-435A-20	Sequence 20, App1
30	14	12.2	23	6	US-10-490-949-47	Sequence 47, App1
31	14	12.2	23	7	US-11-219-563-120	Sequence 120, App1
32	14	12.2	23	7	US-11-251-465-49	Sequence 49, App1
33	14	12.2	23	7	US-11-251-465-59	Sequence 59, App1
34	13	11.3	23	6	US-10-706-435A-15	Sequence 15, App1
35	13	11.3	23	7	US-11-219-563-110	Sequence 110, App1
36	13	11.3	23	7	US-11-251-465-89	Sequence 89, App1
37	13	11.3	23	7	US-11-251-465-113	Sequence 113, App1
38	13	11.3	23	7	US-11-263-057-11	Sequence 11, App1
39	13	11.3	23	7	US-11-251-734-18	Sequence 18, App1
40	13	11.3	23	7	US-11-251-734-19	Sequence 19, App1
41	13	11.3	23	7	US-11-122-986-644	Sequence 644, App1
42	13	11.3	23	7	US-11-122-986-813	Sequence 813, App1
43	12	10.4	23	6	US-10-474-853-16	Sequence 16, App1
44	12	10.4	23	6	US-10-488-015-15	Sequence 15, App1
45	12	10.4	23	6	US-10-511-937-2601	Sequence 2601, App1

ALIGNMENTS

RESULT 1
US-11-251-465-55
Sequence 55, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
TITLE OF INVENTION: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 890
SOFTWARE: PatentIn version 3.3
SEQ ID NO 55
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Protein domain
US-11-251-465-55
Query Match 20.9%; Score 24; DB 7; Length 23;
Best Local Similarity 50.0%; Pred. No. 6e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 5; Conservative 2;
Db 12 GEADAMSIDG 21
5 GLAEGISLSG 14
RESULT 2
US-11-263-057-13
Sequence 13, Application US/11263057
Publication No. US20060094103A1
GENERAL INFORMATION:
APPLICANT: Chou, Kuo-Chen
APPLICANT: Howe, W. Jeffery
TITLE OF INVENTION: Modified BACE
FILE REFERENCE: MBHB 01-1766-A
CURRENT APPLICATION NUMBER: US/11/263,057
CURRENT FILING DATE: 2005-10-31
PRIOR APPLICATION NUMBER: US/10/372,473

```

; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MSC FEATURE
; OTHER INFORMATION: Synthetic peptide substrate with a P33K-BACE cleavage site.
US-11-263-057-13
```

```

Query Match      19.1%; Score 22; DB 7; Length 23;
Best Local Similarity 27.8%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
```

```
QY      6 IAKINGEADAMSLDGSF 23
Db      2 LTNIKTEISEVNLDAEF 19
```

```

RESULT 3
US-10-787-734-11
; Sequence 11, Application US/10787734
; Publication No. US20060115489A1
; GENERAL INFORMATION:
; APPLICANT: BIRKETT, ASHLEY J.
; APPLICANT: FIERIS, WALTER
; TITLE OF INVENTION: INFLUENZA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/91531
; CURRENT APPLICATION NUMBER: US/10/787,734
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/05196
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-787-734-11
```

```

Query Match      16.5%; Score 19; DB 6; Length 23;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 NGEAD 15
Db      19 NGSSD 23
```

```

RESULT 4
US-10-787-734-136
; Sequence 136, Application US/10787734
; Publication No. US20060115489A1
; GENERAL INFORMATION:
; APPLICANT: BIRKETT, ASHLEY J.
; APPLICANT: FIERIS, WALTER
; TITLE OF INVENTION: INFLUENZA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/91531
; CURRENT APPLICATION NUMBER: US/10/787,734
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/05196
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/274,616
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```

; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Influenza
US-10-787-734-136
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```

Query Match      16.5%; Score 19; DB 6; Length 23;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 NGEAD 15
Db      19 NGSSD 23
```

```

RESULT 5
US-10-787-734-139
; Sequence 139, Application US/10787734
; Publication No. US20060115489A1
; GENERAL INFORMATION:
; APPLICANT: BIRKETT, ASHLEY J.
; APPLICANT: FIERIS, WALTER
; TITLE OF INVENTION: INFLUENZA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/91531
; CURRENT APPLICATION NUMBER: US/10/787,734
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/05196
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Influenza
US-10-787-734-139
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```

Query Match      16.5%; Score 19; DB 6; Length 23;
Best Local Similarity 33.3%; Pred. No. 3.5e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      13 EADAMSLDG 21
Db      5 EVDLTRNG 13
```

```

RESULT 6
US-11-252-276-124
; Sequence 124, Application US/11252276
; Publication No. US20060094868A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Bright, Gary
; APPLICANT: Olsson, Keith
; APPLICANT: Butroughs-Tencza, Sarah
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-K2-CO
```



```

; CURRENT APPLICATION NUMBER: US/11/252,276
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: 09/713,572
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/430,656
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/398,965
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 09/031,271
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 08/810,983
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: 60/136,078
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 60/106,308
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Cytoplasm/cytoskeleton target sequence
US-11-252-276-124

Query Match      15.7%; Score 18; DB 7; Length 23;
Best Local Similarity 60.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      17 MSLDG 21
Db      11 LSLEG 15

RESULT 7
US-11-122-986-457
; Sequence 457, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 457
; LENGTH: 23
```

```

; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-457

Query Match      15.7%; Score 18; DB 7; Length 23;
Best Local Similarity 28.6%; Pred. No. 4.9e+03;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      6 IAKIMGEADAMS 19
Db      7 IPIREGAGAGAG 20

RESULT 8
US-09-731-899-21
; Sequence 21, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Diphtheria toxin bacteria
US-09-731-899-21

Query Match      14.8%; Score 17; DB 1; Length 23;
Best Local Similarity 42.9%; Pred. No. 6.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TEDSIK 8
Db      4 TADNLEK 10

RESULT 9
US-10-490-949-36
; Sequence 36, Application US/10490949
; Publication No. US20060093574A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: METHODS FOR EPIOTOPE-SPECIFIC AND CYTOKINE/ANTICYTOKINE
; TITLE OF INVENTION: COMBINATION IMMUNOTHERAPIES FOR MODULATION OF PATHOGENIC
; TITLE OF INVENTION: IMMUNE RESPONSES IN IMMUNE MEDIATED DISEASES
; FILE REFERENCE: UCSID1450-2
; CURRENT APPLICATION NUMBER: US/10/490,949
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/US02/30578
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/339,284
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/325,499
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-490-949-36

Query Match      14.8%; Score 17; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SIAK 8
|||
Db 18 SIAK 21

RESULT 10
US-11-251-465-53
; Sequence 53, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30.172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 53
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein domain
US-11-251-465-53

Query Match 14.8%; Score 17; DB 7; Length 23;
Best Local Similarity 35.7%; Pred. No. 6.9e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 8 KIMGEADAMSING 21
|:|:|
Db 3 KMFGSALCTLTG 16

RESULT 11
US-11-169-140-26
; Sequence 26, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAMLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0

; SEQ ID NO 26
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-140-26

Query Match 14.8%; Score 17; DB 7; Length 23;
Best Local Similarity 60.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 MNGEA 14
|||
Db 13 LMGAA 17

RESULT 12
US-09-949-925-291
; Sequence 291, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 291
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-925-291

Query Match 13.9%; Score 16; DB 1; Length 23;
Best Local Similarity 45.5%; Pred. No. 9.7e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 EDSIAKINGE 13
|||
Db 10 EDERAKIHQTE 20

RESULT 13
US-10-515-429-30
; Sequence 30, Application US/10515429
; Publication No. US20060105387A1
; GENERAL INFORMATION:
; APPLICANT: Pryor, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429

```

:
: CURRENT FILING DATE: 2004-11-23
: PRIOR APPLICATION NUMBER: PCT/US03/26779
: PRIOR FILING DATE: 2003-08-26
: PRIOR APPLICATION NUMBER: US 60/406,977
: PRIOR FILING DATE: 2002-08-30
: PRIOR APPLICATION NUMBER: US 10/384,060
: PRIOR FILING DATE: 2003-03-10
: PRIOR APPLICATION NUMBER: US 66/485,404
: PRIOR FILING DATE: 2003-07-09
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 30
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
: US-10-515-429-30
:

```

Query Match	13.9%	Score 16	DB 6	Length 23
Best local similarity	20.0%	Pred. No.	9.7e+03	
Matches	2	Conservative	4	Mismatches 0
				Gaps 0

```
Qy      8 KIMNGEADAM 17
         :|: | : :
Db      4 EILEGRTECV 13
```

RESULT 14
US-11-219-563-41
; Sequence 41, Application US/11219563
; Publication No. US20060088539A1

? APPLICANT: Bandier, Neil
 ? TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
 ? TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
 ? FILE REFERENCE: 13651.001 (B27-001)
 ? CURRENT APPLICATION NUMBER: US/11/219,563
 ? CURRENT FILING DATE: 2005-09-02
 ? PRIOR APPLICATION NUMBER: PCT/US04/06586
 ? PRIOR FILING DATE: 2004-03-03
 ? PRIOR APPLICATION NUMBER: US 10/379,838
 ? PRIOR FILING DATE: 2003-03-03
 ? PRIOR APPLICATION NUMBER: 10/449,379
 ? PRIOR FILING DATE: 2003-05-30
 ? NUMBER OF SEQ ID NOS: 144
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 41
 ? LENGTH: 23
 ? TYPE: PRT
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: deimmunized light chain J415-5
 ? US-11-219-563-41

Query Match	13.9%	Score 16	DB 7	Length 23
Best Local Similarity	28.6%	Pred. No.	9.7e+03	
Matches	4	Conservative	2	Mismatches 8
				Indels 0
				Gaps 0

```
QY      9  IMNGEADAMSLDGG  22
          :| :||
Db      3  VMTQFPKSMASAG  16
```

RESULT 15
US-11-259-950-21
Sequence 21, Application US/11259956
Publication No. US20060088524A1
GENERAL INFORMATION:
APPLICANT: Morrissey, James
APPLICANT: Pureza, Vincent
APPLICANT: Sliagar, Stephen G.

```

; TITLE OF INVENTION: Tissue Factor Compositions and Methods
; FILE REFERENCE: 46-04
; CURRENT APPLICATION NUMBER: US/11/259,950
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US 60/622,737
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: US 60/536,281
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US 10/465,789
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 11/033,489
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Histey sequence
; US-11-259-950-21

```

Query Match	13.9%	Score 16;	DB 7;	Length 23;
Best Local Similarity	75.0%	Pred. No. 9.7e+03;		
Matches	3;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	TTED	4
		:	
Db	15	TTEN	18

Search completed: June 13, 2006, 02:24:56
Job time : 18 secs

OTHER INFORMATION: HISTEV sequence
US-11-259-950-21

QY	1	TTED	4
		:	
Db	15	TTEN	18

Search completed: June 13, 2006, 02:24:56
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:50:08 ; Search time 97.0588 Seconds
(without alignments)
70.661 Million cell updates/sec

Title: US-10-612-162A-3
Perfect score: 74
Sequence: 1 SKLSWGSGLNLSERN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*
10: geneseqp2006s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	8	ADG46077 Human CDT
2	65	87.8	13	8	ADG46094 Human CDT
3	60	81.1	28	10	AE39171 Human ser
4	60	81.1	28	10	AE39172 Human ser
5	60	81.1	42	8	ADH89392 Human tra
6	60	81.1	42	8	ADK15881 Human tra
7	60	81.1	42	9	ADY54154 Amino aci
8	60	81.1	328	4	AAB84371 Human met
9	60	81.1	575	6	ABR82321 Human met
10	60	81.1	609	8	ABM83782 Human dia
11	60	81.1	627	8	ABM83781 Human dia
12	60	81.1	628	8	ABM83779 Human dia
13	60	81.1	635	8	ADT08174 Human met
14	60	81.1	643	8	ABM83778 Human dia
15	60	81.1	645	8	ABM83783 Human dia
16	60	81.1	646	4	AAU02938 Angiotens
17	60	81.1	646	8	ABM83780 Human dia
18	60	81.1	665	4	AAU02937 Angiotens
19	60	81.1	679	6	ABP72820 Human tra
20	60	81.1	679	8	ADH89360 Human tra
21	60	81.1	679	8	ADK15869 Mature hu
22	60	81.1	679	8	ADL70732 Human tra
23	60	81.1	679	8	ADL24413 Human tra

24	60	81.1	679	8	ADU17885	ADU17885 Human tra
25	60	81.1	679	8	ADT55264	ADT55264 Partial h
26	60	81.1	679	8	ADU07204	ADU07204 Amino aci
27	60	81.1	679	8	ADT78912	ADT78912 Human tra
28	60	81.1	679	8	ADT78149	ADT78149 Human tra
29	60	81.1	679	8	ADT99248	ADT99248 Partial h
30	60	81.1	679	8	ADT36538	ADT36538 Partial h
31	60	81.1	679	8	ADT39423	ADT39423 Human tra
32	60	81.1	679	8	ADU17611	ADU17611 Human tra
33	60	81.1	679	8	ADU17468	ADU17468 Human tra
34	60	81.1	679	8	ADU00630	ADU00630 Human tra
35	60	81.1	679	8	ADT55066	ADT55066 Human par
36	60	81.1	679	9	ADY54149	ADY54149 Amino aci
37	60	81.1	679	9	ADY57102	ADY57102 Human ser
38	60	81.1	679	9	ADY57103	ADY57103 Human ser
39	60	81.1	679	10	AE347501	AE347501 Human tra
40	60	81.1	698	2	AAE12499	AAE12499 Human tra
41	60	81.1	698	2	AAE6492	AAE6492 Human tra
42	60	81.1	698	2	AAW54354	AAW54354 Serotrans
43	60	81.1	698	3	AAI50717	AAI50717 Human ser
44	60	81.1	698	6	ABP72819	ABP72819 Human tra
45	60	81.1	698	7	ADD45282	ADD45282 Human Pro

ALIGNMENTS

RESULT 1
ADG46077
ID ADG46077 standard; peptide; 15 AA.
XX
AC ADG46077;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #3.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN EPI378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 3; 21pp; German.
XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences VVARSWGKEDLWELL, TTEDSTAKINGEADADSLDGF, SKLSWGSGLNLSERN and
XX YEKYLDEEVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for

CC production of antibodies that specifically bind CDR from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDR, which
CC lacks glycosylation at Asn411 and/or Asn 411, is present only in
CC alcohols. The antibodies allow direct detection of CDR in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG45075-ADG46094 represent CDR peptide
CC fragments used in the method of the invention.

SQ Sequence 15 AA;

Query March	100.0%;	Score 74;	DB 8;	Length 15;
Best Local Similarity	100.0%;	Pred. NO. 4e-06;		
Matches 15; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	1	SKL SMGSG LNLSEPN	15
Db	1	SKL SMGSG LNLSEPN	15

RESULT 2
ADG46094
ID ADG46094 standard; peptide; 13 AA.

AC	ADG46094;
XX	
DT	25-MAR-2004 (first entry)

XX	Human CDT peptide fragment #20.
DE	

KM antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholism; diagnosis; human

OS Homo sapiens.

PN EP1378521-A1.

PD 07-JAN-2004

PF 19-MAY-2003; 2003EP-000113334.
YY

PR 05-JUL-2002; 2002DE-01030550.
XX

PA (DADE-) DADE BEHRING MARBURG GMBH.
XX

XX
T1 ALLIUM N;
XX

PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.

PS Example 7; Page 15; 21pp; German.

This invention describes a novel antibody that in aqueous solution, binds selectively to carbohydrate-deficient transferrin (CDT) without having to bind CDT to a solid phase. The invention also describes an antibody that binds selectively to CDT at regions containing the sequences VARSNGGSGEDLIMEL, TIEDSTAKINGSGADMSLDGPF, SKLSWGSGLWLSERN and YKRYDGEYKVKV (ADG46075-ADG46078) and an immunoassay for detecting CDT using the antibodies of the invention. The antibodies of the invention are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The antibodies are obtained by immunisation with non-glycosylated transferrin, or a fragment, then generation of hybridomas by standard fusion of spleen and myeloma cells. Hybridomas are then selected for production of antibodies that specifically bind CDT from the aqueous phase. The antibodies are useful for diagnosis of alcoholism, CDT, which lacks glycosylation at Asn413 and/or Asn 611, is present only in alcoholics. The antibodies allow direct detection of CDT in solution, eliminating the need for immobilising it on a solid phase (as required when using known antibodies). ADG46075-ADG46094 represent CDT peptide fragments used in the method of the invention.

5Q Sequence 13 AA;

Query Match	87.8%	Score 65	DB 8	Length 13
Best Local Similarity	100.0%	Pred. No.	0.00014	
Matches 13	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	3	LSMGSGNLSEPN	15
Db	1	LSMGSGNLSEPN	13

RESULT 3
AEE39171
ID AEE39171 standard; peptide; 28 AA.

AC	AEE39171;
XX	
DT	09-FEB-2006 (first entry)

DE Human serum N-linked glycopeptide SEQ ID NO: 3275.

KM Bionitratics; blood; serum; plasma protein; protein detection;
KM mass spectroscopy; proteomics; glycosylation; diagnosis; cancer;
KM cytosolic; diabetes; antidiabetic; inflammation; antiinflammatory;
KM rheumatoid arthritis; antirheumatic; antirheumatic; psychiatric disorder
KM neuroleptic; neurological disease; infection; antimicrobial.

OS Homo sapiens.

PN W02005114221-A2.

01-DEC-2005
PD

PF 20-MAY-2005; 2005WO-US017842.

PR 21-MAY-2004; 2004US-0573593P.
XX
XXPA (SYSI-) INST SYSTEMS BL
XX

XX
F1 AEBERBOLD KH, ZIANG H,

WFL: 2000-0201/3/02-
XX
XX

PT Identifying glycopolypeptides in a serum or plasma sample, by identifying
PT released sample glycopeptide fragments that correspond to standard
PT peptides.

PS Claim 1; SEQ ID NO 3275; 193pp; English.

CC The invention relates to identifying glycopolypeptides in a serum or
CC plasma sample comprising immobilizing derivatized sample
CC glycopolypeptides to a solid support, releasing the sample glycopeptide
CC fragments from the solid support, adding to the released sample
CC glycopeptide fragments standard peptides, and identifying released sample
CC glycopeptide fragments that correspond to standard peptides added by mass
CC spectroscopy. Also included are a method for identifying one or more
CC diagnostic markers for a disease, a composition comprising peptides
CC containing the glycosylation sites (AEK35897-AEK39378, where the peptides
CC each correspond to peptide fragments derived by cleavage of polypeptides
CC using the same cleavage reagent) and a kit comprising peptides containing
CC the glycosylation sites (AEK35897-AEK39378). The methods are useful for
CC identifying glycopolypeptides in a serum or plasma sample. The methods
CC can be used for blood serum profiling for the detection of prognostic and
CC diagnostic protein markers. It can also be used to identify and/or
CC validate drug targets and to evaluate drug efficacy, drug dosing, and/or
CC drug toxicity. The methods can also be used for the detection of changes
CC in the state of glycosylation of proteins based on the concurrent
CC application of protein abundance measurement of protein glycosylation on
CC the same sample. The method allows fast throughput and simplicity. It can
CC be readily adapted for high throughput analysis of samples, which can
CC particularly advantageous for the analysis of clinical specimens. The
CC method can also be automated to facilitate the processing of multiple
CC samples. The present sequence is a human glycopeptide that does not

CC contain an N-linked glycosylation site, suitable for use as a reference
CC peptide in the method of the invention.

XX
SQ Sequence 28 AA;

Query Match 81.1%; Score 60; DB 10; Length 28;
Best Local Similarity 85.7%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KLSWGSGLNSEPN 15
|||
1 KLCWGSGLNLCPEPN 14

RESULT 4
AEE39172

ID AEE39172 standard; peptide; 28 AA.

XX
AC AEE39172;

XX
DT 09-FEB-2006 (first entry)

XX
DE Human serum N-linked glycopeptide SEQ ID NO: 3276.

XX
KM Bioinformatics; blood; serum; plasma protein; protein detection;
KM mass spectrometry; proteomics; glycosylation; diagnosis; cancer;
KM cytostatic; diabetes; antidiabetic; inflammation; antiinflammatory;
KM rheumatoid arthritis; antiarthritic; antirheumatic; psychiatric disorder;
KM neuroleptic; neurological disease; infection; antimicrobial.

XX
OS Homo sapiens.

XX
PN W02005114221-A2.

XX
PD 01-DEC-2005.

XX
PF 20-MAY-2005; 2005WO-US017842.

XX
PR 21-MAY-2004; 2004US-0573593P.

XX
PA (SYST-) INST SYSTEMS BIOLOGY.

XX
PI Aebersold RH, Zhang H;

XX
DR WPI; 2006-020173/02.

XX
PT Identifying glycopolypeptides in a serum or plasma sample, by identifying
PT released sample glycopeptide fragments that correspond to standard
PT peptides.

XX
PS Claim 1; SEQ ID NO 3276; 193pp; English.

XX
CC The invention relates to identifying glycopolypeptides in a serum or
CC plasma sample comprising immobilizing derivatized sample
CC glycopolypeptides to a solid support, releasing the sample glycopeptide
CC fragments from the solid support, adding to the released sample
CC glycopeptide fragments standard peptides, and identifying released sample
CC glycopeptide fragments that correspond to standard peptides added by mass
CC spectroscopy. Also included are a method for identifying one or more
CC diagnostic markers for a disease, a composition comprising peptides
CC containing the glycosylation sites (AEE35897-AEE39378, where the peptides
CC each correspond to peptide fragments derived by cleavage of polypeptides
CC using the same cleavage reagent) and a kit comprising peptides containing
CC the glycosylation sites (AEE35897-AEE39378). The methods are useful for
CC identifying glycopolypeptides in a serum or plasma sample. The method
CC can be used for blood serum profiling for the detection of prognostic and
CC diagnostic protein markers. It can also be used to identify and/or
CC validate drug targets and to evaluate drug efficacy, drug dosing, and/or
CC drug toxicity. The methods can also be used for the detection of changes
CC in the state of glycosylation of proteins based on the concurrent
CC application of protein abundance measurement of protein glycosylation on
CC the same sample. The method allows fast throughput and simplicity. It can
CC be readily adapted for high throughput analysis of samples, which can be

CC particularly advantageous for the analysis of clinical specimens. The
CC method can also be automated to facilitate the processing of multiple
CC samples. The present sequence is a human glycopeptide that does not
CC contain an N-linked glycosylation site, suitable for use as a reference
CC peptide in the method of the invention.

XX
SQ Sequence 28 AA;

Query Match 81.1%; Score 60; DB 10; Length 28;
Best Local Similarity 85.7%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KLSWGSGLNSEPN 15
|||
1 KLCWGSGLNLCPEPN 14

RESULT 5
ADH89392

ID ADH89392 standard; protein; 42 AA.

XX
AC ADH89392;

XX
DT 15-APR-2004 (first entry)

XX
DE Human transferrin protein domain SegID36.

XX
KM fusion protein; transferrin protein; glycosylation;
KM antibody variable region; cytostatic; antibacterial; virucide;
KM antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KM septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
KM viral infection; parasitic infection; neoplasm; autoimmune disease;
KM arthritis; graft rejection; human.

XX
OS Homo sapiens.

XX
PN US2003226155-A1.

XX
PD 04-DEC-2003.

XX
PF 10-MAR-2003; 2003US-00384060.

XX
PR 30-AUG-2001; 2001US-0315745P.

XX
PR 30-NOV-2001; 2001US-0334059P.

XX
PR 30-AUG-2002; 2002US-00231494.

XX
PR 30-AUG-2002; 2002US-0406977P.

XX
PA (BIOR-) BIOREXIS PHARM CORP.

XX
PI Sadeghi H, Prior CP, Turner A;

XX
DR WPI; 2004-022093/02.

XX
PT New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.

XX
PS Example 2; SEQ ID NO 36; 82pp; English.

XX
CC This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a domain of the human transferrin protein which was
CC used in the exemplification of the invention.

```
XX
SQ Sequence 42 AA:
Query Match      81.1%; Score 60; DB 8; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0042;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGGLNLSEPN 15
      ||| ||| ||| ||| |||
Db      25 KLCMGSGGLNLCEPN 38

RESULT 6
ADK15881
ID ADK15881 standard; protein; 42 AA.
XX
AC ADK15881;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human transferrin (Tf) protein fragment #3.
XX
KW fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
KM glucagons-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
KM T-20; soluble toxin receptor; epitope tagging; human.
XX
OS Homo sapiens.
XX
PN US2003221201-A1.
XX
PD 27-NOV-2003.
XX
PF 04-MAR-2003; 2003US-00378094.
XX
PR 30-AUG-2001; 2001US-0315745P.
PR 30-NOV-2001; 2001US-0334059P.
PR 30-AUG-2002; 2002US-00231494.
PR 30-AUG-2002; 2002US-0406977P.
XX
PA (BIOR-) BIOREXIS PHARM CORP.
XX
PI Prior CP, Lai C, Sadeghi H, Turner A;
XX
WPI; 2004-010899/01.
XX
PT New fusion protein comprising a modified transferrin (Tf) protein fused
PT to a therapeutic protein or peptide, useful for epitope tagging.
XX
PS Example 5; SEQ ID NO 15; 70pp; English.
XX
CC The invention comprises a fusion protein that contains a modified
CC transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.
CC beta-interferon - IFN, glucagons-like peptide - GLP-1, erythropoietin
CC mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
CC protein of the invention is useful for epitope tagging. The present amino
CC acid sequence represents a fragment of the human Tf protein.
XX
SQ Sequence 42 AA:
Query Match      81.1%; Score 60; DB 8; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0042;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGGLNLSEPN 15
      ||| ||| ||| ||| |||
Db      25 KLCMGSGGLNLCEPN 38

RESULT 7
ADY54154
ID ADY54154 standard; peptide; 42 AA.
XX
AC ADY54154;
```

```
XX
DT 19-MAY-2005 (first entry)
XX
DE Amino acid sequence of C1 subdomain of human transferrin.
XX
KW cytosstatic; anti-HIV; hypotensive; neuroprotective; cardiovascular-Gen.;
KW nootropic; hepatotropic; vitucide; antiinflammatory; immunosuppressive;
KW antiallergic; antimicrobial; neuroleptic; gynecological; anorectic;
KW antiarteriosclerotic; gastrointestinal-Gen.; endocrine-Gen; neoplasm;
KW hematological disease; transferrin; erythropoietin peptide mimetic; EPM;
KW EPO mimetic peptide-1; EMP-1; multiple sclerosis; brain tumor; cancer;
KW hepatitis; anemia; pregnancy; menstrual disorder; rheumatoid arthritis;
KW AIDS; viral disease; metabolic disease; autoimmune disease;
KW inflammatory disease; allergy; microbial infection;
KW cardiovascular disease; genetic disease; neurodegenerative disease;
KW hematopoietic cell disorder; endocrine disorder;
KW gastrointestinal disease; hypertension; arterial sclerosis.
XX
OS Homo sapiens.
XX
PN WO2005021579-A2.
XX
PD 10-MAR-2005.
XX
PF 30-AUG-2004; 2004MO-US027949.
XX
PR 28-AUG-2003; 2003MO-US026818.
PR 10-MAR-2004; 2004US-0551552P.
XX
PA (BIOR-) BIOREXIS PHARM CORP.
XX
PI Sadeghi H, Turner AJ;
XX
WPI; 2005-214540/22.
XX
DR Novel erythropoietin (EPO) peptide mimetic, having first modification of
PT cysteine residue of EPO mimetic peptides (EMP)-1, to reduce disulfide
PT bond formation, and second modification such that peptide exhibits EMP-1
PT activity.
XX
PS Example 1; SEQ ID NO 8; 158pp; English.
XX
CC The specification describes an erythropoietin (EPO) peptide mimetic
CC (EPM), comprising a modification of at least one cysteine residue of EPO
CC mimetic peptide (EMP)-1 that substantially reduces disulfide bond
CC formation, and a second modification comprising the deletion or substitution
CC of at least one cysteine residue in EMP-1, and the second modification
CC comprises the addition of a linker group that is covalently bonded to the
CC C-terminal amino acid or N-terminal amino acid of EMP-1. EPM peptides of
CC the invention are useful for treating or preventing diseases, such as
CC multiple sclerosis, brain tumor, skin cancer, hepatitis B, hepatitis C,
CC anemia, beta-thalassemia, pregnancy or menstrual disorders, rheumatoid
CC arthritis, AIDS, cancer, viral disease, metabolic disease, obesity,
CC autoimmune disease, inflammatory disease, allergy, graft-versus-host
CC disease, systemic microbial infection, cardiovascular disease, psychosis,
CC genetic diseases, neurodegenerative diseases, disorders of hematopoietic
CC cells, diseases of the endocrine system or reproductive systems,
CC gastrointestinal diseases, diabetes, asthma, or HIV infections,
CC hypertension, hypercholesterolemia, arterial sclerosis, arthritis or
CC Alzheimer's disease. The present sequence represents the C1 subdomain of
CC human transferrin. A fusion protein, with increased half life, comprising
CC an EPM peptide and modified transferrin is used in the course of the
CC invention.
XX
SQ Sequence 42 AA:
Query Match      81.1%; Score 60; DB 9; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0042;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGGLNLSEPN 15
      ||| ||| ||| ||| |||
```


Db 25 KLCWGSGLNLCERN 38

RESULT 8
ID AAB84371 standard; protein: 328 AA.

XX
AC AAB84371;
XX
DT 22-AUG-2001 (first entry)
XX
DE Amino acid sequence of a human transferrin.

XX
KM Human; transferrin; autoimmune disease; rheumatoid arthritis;
KM hyperproliferative disorder; neoplasm; cardiovascular disorder;
KM cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KM ocular disorder; corneal infection; wound healing;
KM epithelial cell proliferation; aging; organ transplant.

XX
OS Homo sapiens.
XX
PN MO200146254-A1.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-US034769.
XX
PR 23-DEC-1999; 99US-0171595P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Shi Y, Choi GH;
XX
DR WPI; 2001-381910/40.
DR N-PSDB; AAH25190.
XX
PT Isolated nucleic acid molecule encoding a human tranferrin protein is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Claim 11; Page 286-287; 290pp; English.

XX
CC The present sequence represents human transferrin polypeptide.
CC Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver.
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC alzheimer's disease, corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities

XX
SQ Sequence 328 AA;

QY Query Match 81.1%; Score 60; DB 4; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.042;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 KLSWGSGLNLCERN 15
179 KLCWGSGLNLCERN 192

RESULT 9
ID ABR82321 standard; protein: 575 AA.

AC ABR82321;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human metalloprotein (MEPR) polypeptide (id=7509328CD1).
XX
KM MEPR; metalloprotein; anti-HIV; antifibrotic; antiinflammatory; human;
KM antianemic; antiparkinsonian; neurotropic; anticonvulsant; cyrostatic;
KM antiarteriosclerotic; antiaschmatic; immunosuppressive; antithyroid;
KM hepatotropic; dermatological; antidiabetic; nephrotropic; antigout;
KM thymometric; neuroprotective; osteopathic; antiarthritic; uropathic;
KM antiparasitic; antihelminthic; antiseptic; ophthalmological; virucide;
KM antirheumatic; haemostatic; antibacterial; protozoacide; fungicide;
KM gene therapy; transgenic.

XX
OS Homo sapiens.
XX
PN MO2003060089-A2.
XX
PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001485.
XX
PR 14-JAN-2002; 2002US-0348769P.
PR 16-JAN-2002; 2002US-0350701P.
PR 19-MAR-2002; 2002US-036059P.
PR 10-MAY-2002; 2002US-0379907P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Kable AE, Griffin JA, Gervad AE, Becha SD, Richardson TW;
PI Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Marquis JP;
PI Tang YT;
XX
DR WPI; 2003-539823/56.
DR N-PSDB; ACF35812.
XX
PT New human metalloproteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
PT hepatitis.

XX
PS Claim 1; Page 146-148; 153pp; English.

XX
CC The invention relates to novel human metalloproteins (MEPR) and encoding
CC polynucleotides. The human MEPR polypeptides, polynucleotides and
CC modulators are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MEPR, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding MEPR are useful for creating transgenic animals
CC to model human disease. Sequences ABR82316-323 represent the human MEPR
CC polypeptides of the invention

XX
SQ Sequence 575 AA;

QY Query Match 81.1%; Score 60; DB 6; Length 575;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 KLSWGSGLNLCERN 15
392 KLCWGSGLNLCERN 405

RESULT 10
 ABM83782
 ID ABM83782 standard; protein; 609 AA.
 XX
 AC ABM83782;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4031.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 XX
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patuty S, Shi X, Suarez CJ;
 XX
 DR MPI; 2004-329368/30.
 DR N-PSDB; ACN42434.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorder, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The ditnp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a ditnp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 609 AA;
 XX
 QY Query Match 81.1%; Score 60; DB 8; Length 609;
 DB Best Local Similarity 85.7%; Pred. No. 0.084; Mismatches 0; Gaps 0;
 Matches 12; Conservative 0; Indels 2; Indels 0; Gaps 0;
 2 KLSMSGGLNISEPN 15
 444 KLCMSGGLNICEPN 457

RESULT 11
 ABM83781
 ID ABM83781 standard; protein; 627 AA.
 XX
 AC ABM83781;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 XX
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patuty S, Shi X, Suarez CJ;
 XX
 DR MPI; 2004-329368/30.
 DR N-PSDB; ACN42433.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorder,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorder, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The ditnp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a ditnp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 627 AA;
 XX
 QY Query Match 81.1%; Score 60; DB 8; Length 627;
 DB Best Local Similarity 85.7%; Pred. No. 0.087; Mismatches 0; Gaps 0;
 Matches 12; Conservative 0; Indels 2; Indels 0; Gaps 0;
 2 KLSMSGGLNISEPN 15
 444 KLCMSGGLNICEPN 457

RESULT 12

ABM83779

ID ABM83779 standard; protein; 628 AA.

AC ABM83779;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4028.

KM gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.

XX Homo sapiens.

XX MO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003MO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Hartshorne TA, Suchotolski MT, Altus CM, Plets SD, Elder LV;

XX Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;

XX Stevens KA, Blanchard JL, Panzer SR, Mang X, Au AP, Gerstein EH;

XX Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;

XX Lagace RE, Spito PA, Stewart EA, Wingrove J, Vite UA, Kitron ES;

XX Xu Y, Kwong M, Plickly JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Faty S, Shi X, Suarez CJ;

XX WPI: 2004-329368/30.

XX N-PSDB; ACN42431.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX in diagnosing a condition, disease or disorder associated with human

XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

XX polynucleotide of the invention may have a use in gene therapy. The human

XX diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be

XX used to diagnose a particular condition, disease or disorder associated

XX with human molecules, e.g. cell proliferative disorders,

XX autoimmune/inflammatory disorder, developmental disorder, endocrine

XX infection caused by virus, bacteria, fungi or parasite. The ditnp

XX molecules may also be used in genetic mapping, in identifying individuals

XX from minute biological samples, in detecting single nucleotide

XX polymorphisms, as molecular weight markers, and for somatic or germline

XX gene therapy. The present sequence data for this patent is not represented in

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 628 AA;

XX Query Match 81.1%; Score 60; DB 8; Length 628;

XX Best Local Similarity 85.7%; Pred. No. 0.087;

XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 2 KLSWGSGLNLEPN 15

XX 463 KLCWGSGLNLEPN 476

XX RESULT 13

ADT08174

ID ADT08174 standard; protein; 635 AA.

AC ADT08174;

DT 30-DEC-2004 (first entry)

DE Human metal binding protein (MBP) (ID: 7512697CD1).

KM MBP; metal binding protein; cytosolic; antiarteriosclerotic;

XX anticonvulsant; neurotrophic; neuroprotective; cerebroprotective; anti-HIV;

XX antiallergic; antiinflammatory; thymomimetic; transgenic; human.

XX Homo sapiens.

XX MO2004085612-A2.

XX 07-OCT-2004.

XX 17-MAR-2004; 2004MO-US008328.

XX 24-MAR-2003; 2003US-0457538P.

XX (INCY-) INCYTE CORP.

XX Jiang X, Jackson AA, Hafalia AJA, Mason PM;

XX WPI: 2004-710307/69.

XX N-PSDB; ADT08177.

XX New human metal binding proteins (MBP), useful for diagnosing, treating

XX and preventing diseases or conditions associated with the aberrant MBP

XX expression e.g. cancer, AIDS, epilepsy, or infections.

XX Claim 1; SEQ ID NO 3; 161pp; English.

XX The invention relates to novel human metal binding proteins (MBP) and

XX encoding polynucleotides. The MBPs can be expressed by standard

XX recombinant methodology. The polypeptides and polynucleotides are useful

XX in diagnosing, treating and preventing diseases or conditions associated

XX with the decreased expression or overexpression of MBP, such as cell

XX proliferative (e.g. cancer, atherosclerosis), neurological (e.g.

XX epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,

XX allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)

XX disorders, or infections. These are also useful in assessing the effects

XX of exogenous compounds on the expression of nucleic acid and amino acid

XX sequences of MBP. The MBP or its fragments are useful in screening

XX compounds for effectiveness as agonist or antagonist of the polypeptides,

XX or in altering the expression of the target polynucleotide and compounds

XX that specifically bind to or modulate the activity of the polypeptide. An

XX microarray comprising different nucleotide molecules affixed at distinct

XX physical locations on a solid substrate, where at least one nucleotide

XX molecule comprises a first oligonucleotide or polynucleotide sequence

XX specifically hybridizable with at least 30 contiguous nucleotides of the

XX target polynucleotide is useful in monitoring or measuring protein-

XX protein interactions, drug-target interactions, and gene expression

XX profiles. The present sequence represents a human MBP.

XX Sequence 635 AA;

XX Query Match 81.1%; Score 60; DB 8; Length 635;

XX Best Local Similarity 85.7%; Pred. No. 0.088;

XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 2 KLSWGSGLNLEPN 15

XX 452 KLCWGSGLNLEPN 465

XX RESULT 14

XX ABM83778

XX ID ABM83778 standard; protein; 643 AA.

[illegible]

```

XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pproteins SEQ ID NO:4032.
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX Hathesorne TA, Suchorolski MT, Altus CM, Pites SU, Elder LV;
XX Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
XX Petralia CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX LePage RE, Spito PA, Stewart EA, Wingrove J, Vite UA, Kirtton ES;
XX Xu Y, Kwong M, Policky CJ, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
XX Patency S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
XX
XX N-PSDB; ACN42435.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 27, Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The ditnp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a ditnp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 645 AA:
XX
XX Query Match 81.1%; Score 60; DB 8; Length 645;
XX Best Local Similarity 85.7%; Pred. No. 0.09;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX
XX 2 KLSMGSGLNLEPN 15
XX |||||||
XX |||||||
XX 462 KLCMGSGNLNLEPN 475

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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:18:14 ; Search time 15.2206 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-3
Perfect score: 74
Sequence: 1 SKLSMGSGLNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	1	TFHUP
2	41	55.4	148	2	C65068
3	41	55.4	163	2	C91092
4	41	55.4	163	2	G85937
5	40	54.1	382	2	T13474
6	40	54.1	384	2	T13469
7	40	54.1	400	1	SAVLA
8	40	54.1	400	2	S35528
9	40	54.1	445	2	S43492
10	40	54.1	448	2	D71852
11	40	54.1	448	2	H64663
12	39	52.7	516	2	T27845
13	39	52.7	338	2	C89991
14	39	52.7	400	1	QJ1575
15	39	52.7	400	1	SAVLKS
16	39	52.7	400	1	SAVLVD
17	39	52.7	494	2	T02523
18	39	52.7	545	2	UC2500
19	39	52.7	610	2	A96701
20	39	52.7	915	2	S24577
21	39	52.7	1268	2	AB0204
22	39	52.7	3828	2	T13857
23	38	51.4	289	2	T48108
24	38	51.4	293	2	T40702
25	38	51.4	311	2	T42088
26	38	51.4	316	2	T49376
27	38	51.4	317	1	S67781
28	38	51.4	322	2	S43453
29	38	51.4	465	2	G90961

30	38	51.4	465	2	G85809	flagellar capping
31	38	51.4	468	2	A64956	flagellar hook-ans
32	38	51.4	768	2	AH1085	hypothetical prote
33	38	51.4	769	1	W2B854	gene 54 protein -
34	38	51.4	1021	2	T05901	hypothetical prote
35	38	51.4	2212	2	A41098	calcium channel pr
36	37.5	50.7	431	2	P95236	PRS system, IIC co
37	37.5	50.7	431	2	H98100	hypothetical prote
38	37	50.0	106	2	T20860	hypothetical prote
39	37	50.0	124	2	B27632	T-cell receptor al
40	37	50.0	152	2	F71973	hypothetical prote
41	37	50.0	282	2	S31463	probable integrase
42	37	50.0	325	2	T35318	probable dehydroge
43	37	50.0	335	2	C95118	hypothetical prote
44	37	50.0	335	2	A97968	hypothetical prote
45	37	50.0	344	1	FWRTC2	T-cell surface gly

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor [validated] - human
N:Alternate names: siderophilin
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A20981; A92417; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A03
R:Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; Van Bragt, P.H.; Baldwin
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A:Title: Human transferrin: cDNA characterization and chromosomal localization.
A:Reference number: A20981; MUID:84194084; PMID:6565826
A:Contents: variant C
A:Accession: A20981
A:Molecule type: mRNA
A:Residues: 1-698 <YAN>
A:Cross-references: UNIPROT:P02787; UNIPARC:UPI00002F089; EMBL:M12530; NID:G339452; PID
A>Note: the authors translated the codon CAA for residue 203 as Glu
R:MacGillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Linback-Zins, J.; Brew,
J. Biol. Chem. 258, 3543-3553, 1983
A:Title: The primary structure of human serum transferrin. The structures of seven cyano-
A:Reference number: A92417; MUID:83160878; PMID:6833213
A:Accession: A92417
A:Molecule type: protein
A:Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-
A:Cross-references: UNIPARC:UPI0000174483
A>Note: the sequence shown is the predominant electrophoretic genetic variant (C or T/C)
R:Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakim, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3148-3153, 1985
A:Title: Organization of the human transferrin gene: direct evidence that it originated
A:Reference number: A94044; MUID:85216459; PMID:3858812
A:Accession: A94044
A:Molecule type: DNA
A:Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A:Cross-references: UNIPARC:UPI0000174484; EMBL:M11361
R:Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A:Title: The human transferrin gene: 5' region contains conserved sequences which match
A:Reference number: A29090; MUID:87192006; PMID:3106157
A:Accession: A29090
A:Molecule type: DNA
A:Residues: 1-72, 291-300 <ADR>
A:Cross-references: UNIPARC:UPI000016B0AC; UNIPARC:UPI000016B0AD; EMBL:M15673
R:Uzan, G.; Fraim, M.; Park, I.; Besmond, C.; Maessen, G.; Trepac, J.S.; Zakim, M.M.; Ka
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A:Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A:Reference number: A32739; MUID:84153910; PMID:6322780
A:Accession: A32739
A:Molecule type: mRNA
A:Residues: 422-690, 'G', 692-698 <UZA>
A:Cross-references: UNIPARC:UPI000016B0AB; EMBL:M15525; NID:G339468; PIDN:AAA61142.1; PI
R:MacGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Linback-Zins, J.; Brew,

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Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982
A>Title: The complete amino acid sequence of human serum transferrin.
A/Reference number: A93911; MUID:922216; PMID:6953407
A/Contents: annotation; disulfide bonds
R/Hersheberger, C.L.; Larson, J.L.; Arnold, B.; Roestek, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A/Reference number: I51959; MUID:92231399; PMID:1809186
A/Accession: I51959
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-698 <RES>
A/Cross-references: UNIPARC:UPI000002P089; GB:S95936; NID:G248647; PIDN:AA622049.1; PID:
R/Puguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A/Reference number: I48174; MUID:89386721; PMID:2780570
A/Accession: I63133
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 636-696 <RE2>
A/Cross-references: UNIPARC:UPI000016B13C; GB:M26641; NID:G339988; PIDN:AAA61233.1; PID:
R/Scheeff, E.; Lucero, M.A.; Jeltsch, J.M.; Py, M.C.; Levin, M.J.; Champon, P.; Cohen,
Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A/Reference number: I54011; MUID:88056305; PMID:3678832
A/Accession: I54011
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-72 <RE3>
A/Cross-references: UNIPARC:UPI000016B0AC; GB:M17611; NID:G339480; PIDN:AAA61147.1; PID:
A/Accession: I68160
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 564-698 <RE4>
A/Cross-references: UNIPARC:UPI000016B0AE; GB:M17614; NID:G339483; PIDN:AAA61148.1; PID:
A/Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C/Genetic:
A/Gene: GDB:TF
A/Cross-references: GDB:I20432; OMIM:190000
A/Map position: 3q21-3q21
A/Intons: 15/1; 72/3; 119/1; 168/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
C/Function:
A>Description: binds iron for delivery into cells
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-698/Product: transferrin #status experimental <MAT>
F:20-350/Domain: transferrin repeat homology <TRH1>
F:356-686/Domain: transferrin repeat homology <TRH2>
F:68-67;38-58;13-213;156-350;177-193;180-196;190-198;246-260;358-615;364-396;374-387;42
F:432;630/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 81.4%; Score 60; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNISEPN 15
DB 515 KLCMGSGNLNCEPN 528

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A/Accession: C65068
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-148 <BLAT>
A/Cross-references: UNIPROT:Q46786; UNIPARC:UPI000013B063; GB:AE000369; GB:U00096; NID:92
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNISE 13
DB 35 KITMGSGLNYIE 46
RESULT 3
hypothetical protein ECe3707 (imported) - Escherichia coli (strain O157:H7, substrain R1
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
A/Accession: C91092
R/Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A/Reference number: A9629; MUID:2156231; PMID:11258796
A/Accession: C91092
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-163 <NAV>
A/Cross-references: UNIPROT:Q8X6H8; UNIPARC:UPI000000DB83; GB:BA000007; PIDN:BA837130.1;
A/Experimental source: strain O157:H7, substrain RMD 050952
C/Genetic:
A/Gene: ECe3707
C/Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 163;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNISE 13
DB 35 KITMGSGLNYIE 46
RESULT 4
hypothetical protein Z4171 (imported) - Escherichia coli (strain O157:H7, substrain EDL9
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A/Accession: G85937
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousie, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: G85937
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-163 <SNO>
A/Cross-references: UNIPROT:Q8X6H8; UNIPARC:UPI000000DB83; GB:AE005174; NID:G12517343; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetic:
A/Gene: Z4171
C/Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 163;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNISE 13

```

Db 35 KITMSGCLNTRYE 46

RESULT 5

T13474 large surface antigen - hepatitis B virus (isolate 29Y11HCC)

N:Alternate names: envelope protein; Hbs antigen

N:Contains: major surface antigen; middle surface antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate 29Y11HCC

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 31-Dec-2004

C:Accession: T13474

R:Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishihiro, S.

Arch. Virol. 143, 2313-2326, 1998

A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin

A:Reference number: 217684; PMID:99129050; PMID:9930189

A:Accession: T13474

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-382 <TK>

A:Cross-references: UNIPROT:Q9YZS2; UNIPARC:UPI0000178419; EMBL:AB014388; NID:G3582361;

A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 29Y11HCC

C:Genetics:

A:Gene: S

A:Introns: 123/2

C:Keywords: glycoprotein; surface antigen

Query Match 54.1%; Score 40; DB 2; Length 382;

Best Local Similarity 60.0%; Pred. No. 21;

Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 SKLMSGCLNISEPN 15

6 SKPRQGMGTNLSPN 20

RESULT 6

T13469 large surface antigen - hepatitis B virus (isolate 09D09HCC)

N:Alternate names: envelope protein

N:Contains: major surface antigen; middle surface antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate 09D09HCC

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13469

R:Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishihiro, S.

Arch. Virol. 143, 2313-2326, 1998

A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin

A:Reference number: 217684; PMID:99129050; PMID:9930189

A:Accession: T13469

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-384 <TK>

A:Cross-references: UNIPROT:Q9YZU2; UNIPARC:UPI00000FLC85; EMBL:AB014368; NID:G35511304;

A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HCC

C:Genetics:

A:Gene: S

A:Introns: 123/2

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: glycoprotein; surface antigen

Query Match 54.1%; Score 40; DB 2; Length 384;

Best Local Similarity 60.0%; Pred. No. 21;

Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 SKLMSGCLNISEPN 15

6 SKPRQGMGTNLSPN 20

RESULT 7

SAVLA

large surface antigen - hepatitis B virus (subtype adr)

N:Contains: major surface antigen; middle surface antigen

C:Species: hepatitis B virus, HBV

C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004

C:Accession: A03705; S04569; J02107; P00608

R:Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Sugino, Y.; Nishioh, K.

Nucleic Acids Res. 11, 1747-1757, 1983

A:Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype

A:Reference number: A93460; PMID:85168919; PMID:6300776

A:Accession: A03705

A:Molecule type: DNA

A:Residues: 1-400 <NO>

A:Cross-references: UNIPROT:P03140; UNIPARC:UPI00001389C1; GB:V00867

R:Rho, H.M.; Kim, K.; Hyun, S.W.; Kim, Y.S.

Nucleic Acids Res. 17, 2124, 1989

A:Title: The nucleotide sequence and reading frames of a mutant hepatitis B virus subtyp

A:Reference number: S04568; PMID:89183619; PMID:2928116

A:Accession: S04569

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-50, 'R', 52-66, 'YP', 69-129, 'V', 131-142, 'P', 144-164, 'S', 166-176, 'S', 178-338, '

A:Cross-references: UNIPARC:UPI000017496C; EMBL:X14193

R:Notder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouge, A.M.; Mushahwar, I.K.; Magnus,

J. Gen. Virol. 74, 1341-1348, 1993

A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin

A:Reference number: J02044; PMID:93329382; PMID:8336122

A:Accession: J02107

A:Molecule type: DNA

A:Residues: 175-400 <NOR>

A:Cross-references: UNIPARC:UPI0000033737

A:Experimental source: genogroup C, subtype adr, strain pRBHbadr4

R:Notder, H.; Courouge, A.M.; Magnus, L.O.

J. Gen. Virol. 73, 3141-3145, 1992

A:Title: Molecular basis of hepatitis B virus serotype variations within the four major

A:Reference number: P00453; PMID:93107848; PMID:1469353

A:Accession: P00608

A:Molecule type: DNA

A:Residues: 275-354 <NO2>

A:Cross-references: UNIPARC:UPI000017496D

A:Experimental source: subtype adrq+, Bau

C:Genetics:

A:Gene: pre-S1/pre-S2/S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: glycoprotein; surface antigen (gene pre-S2/S) #status predicted <DSa>

F:120-400/Product: middle surface antigen (gene S) #status predicted <MSa>

F:175-400/Product: major surface antigen (gene S) #status predicted

F:15,123,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.1%; Score 40; DB 1; Length 400;

Best Local Similarity 60.0%; Pred. No. 22;

Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 SKLMSGCLNISEPN 15

6 SKPRQGMGTNLSPN 20

RESULT 8

S35528 large surface antigen - hepatitis B virus (subtype adr)

N:Alternate names: envelope protein; Hbs antigen

N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid

C:Species: hepatitis B virus, HBV

A:Variety: subtype adr

C>Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S35528

R:Mukai, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hiji, K.

Nucleic Acids Res. 20, 6105, 1992

A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SHDR) and

A:Reference number: S35527; PMID:93096607; PMID:1461746

A:Accession: S35528

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-400 <MUK>
 A:Cross-references: UNIPROT:Q81108; UNIPARC:UPI00000F044D; EMBL:DJ2980; NID:G221500; PII
 A:Experimental source: subtype adr
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 C:Genetics:
 A:Gene: S
 A:Introns: 165/2
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen
 F:1-400/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
 F:1-119/Domin: pre-S1 domain #status predicted <PRE1>
 F:120-400/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F
 F:120-174/Domin: pre-S2 domain #status predicted <PRE2>
 F:175-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 54.1%; Score 40; DB 2; Length 400;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SKLMSGSLNLESPN 15
 DB 6 SKPRQGMGTLSVFN 20

RESULT 9
 S43492
 Surface antigen - hepatitis B virus (subtype adr)
 N:Alternate names: Hbs antigen
 N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
 C:Species: hepatitis B virus, HBV
 A:Variety: subtype adr
 C:Date: 07-Sep-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S43492; PNO601; PNO602
 R:Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
 Nucleic Acids Res. 18, 4940, 1990
 A:Title: Sequence of a replication competent hepatitis B virus genome with a prex open r
 A:Reference number: S12598; MUID:90370503; PMID:2395664
 A:Accession: S43492
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-445 <LON>
 A:Cross-references: UNIPROT:Q67953; UNIPARC:UPI00000F18F0; EMBL:X52939; NID:G457780; PII
 A:Experimental source: subtype adr
 R:Mims, L.T.; Solomon, L.R.; Ebert, J.W.; Fields, H.
 Blochem. Biophys. Res. Commun. 195, 186-191, 1993
 A:Title: Unique pres sequence in a gibbon-derived hepatitis B virus variant.
 A:Reference number: PNO601; MUID:93371402; PMID:8363598
 A:Accession: PNO601
 A:Molecule type: protein
 A:Residues: 57-95 <MIM>
 A:Cross-references: UNIPARC:UPI0000178459
 A:Accession: PNO602
 A:Molecule type: protein
 A:Residues: 165-196 <MIZ>
 A:Cross-references: UNIPARC:UPI0000178459
 C:Genetics:
 A:Gene: S
 A:Introns: 210/3
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen
 F:1-445/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
 F:1-164/Domin: pre-S1 domain #status predicted <PRE1>
 F:165-445/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F
 F:165-219/Domin: pre-S2 domain #status predicted <PRE2>
 F:220-445/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 54.1%; Score 40; DB 2; Length 445;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SKLMSGSLNLESPN 15
 DB 51 SKPRQGMGTLSVFN 65

RESULT 10
 D71852
 probable signal recognition particle protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: D71852
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathc
 A:Reference number: A71800; MUID:9910557; PMID:9923682
 A:Accession: D71852
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-448 <ARN>
 A:Cross-references: UNIPROT:Q92K62; UNIPARC:UPI0000135EDF; GB:AE001535; GB:AE001439; NID
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: ftn
 C:Superfamily: signal recognition particle 54K protein

Query Match 54.1%; Score 40; DB 2; Length 448;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNLESPN 15
 DB 394 RIALGSGLEVSSEIN 407

RESULT 11
 H64663
 signal recognition particle protein - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: H64663
 R:Tom, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Flatemann, R.D.;
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Kralak, H.G.; Glöde, A.; McKenney
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.H
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: H64663
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-448 <TOM>
 A:Cross-references: UNIPROT:P56005; UNIPARC:UPI0000135EDF; GB:AE000621; GB:AE000511; NID
 C:Superfamily: signal recognition particle 54K protein

Query Match 54.1%; Score 40; DB 2; Length 448;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNLESPN 15
 DB 394 RIALGSGLEVSSEIN 407

RESULT 12
 T27845
 hypothetical protein ZK402.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27845
 R:Favell, T.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid ZK402.
 A:Reference number: Z20429
 A:Accession: T27845

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <FAV>
A;Cross-references: UNIPROT:Q23477, UNIPARC:UPI00000783D4, EMBL:U40956; PIDN:AAA81756.1;
C;Genetics:
A;Gene: CESP:ZK402.5
A;Introns: 28/2; 122/2; 160/2; 248/2; 420/3
C;Superfamily: Caenothabditis elegans hypothetical protein Y57A10A.h
Query Match 54.1%; Score 40; DB 2; Length 516;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 2 SKLMSGGLNISEPN 14
Db 476 KIRGCGGLNSPP 488
RESULT 13
C89991
hypothetical protein SA1812 (imported) - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89991
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89991
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <KIR>
A;Cross-references: UNIPROT:Q99SN8, UNIPARC:UPI00000CACAB; GB:BA000018; PID:g13701799; E
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1812
C;Superfamily: leukocidin
Query Match 52.7%; Score 39; DB 2; Length 338;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 SKLMSGGLNISEPN 15
Db 86 AKGTIGGLRLDPN 100
RESULT 14
JQ1575
major surface antigen - hepatitis B virus
N;Alternate names: envelope protein; HBs antigen
N;Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: S47411; JQ1575
R;Pucieniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolat
A;Reference number: S47404
A;Accession: S47411
A;Molecule type: DNA
A;Residues: 1-400 <PLU>
A;Cross-references: UNIPROT:Q67896, UNIPARC:UPI00000F5BAF; EMBL:Z35717; NID:G527440; PII
A;Experimental source: subtype adw2
R;Norder, H.; Hammas, B.; Loeffel, S.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
A;Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis
A;Reference number: JQ1570; MUID:92268879; PMID:1588323
A;Accession: JQ1575
A;Molecule type: DNA

A;Residues: 175-400 <NOR>
A;Cross-references: UNIPARC:UPI00000002E4; GB:X75666; NID:g416074; PIDN:CAA53362.1; PID:
A;Experimental source: subtype adw2, strain p6
C;Genetics:
A;Gene: S
A;Introns: 122/3
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;1-400/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F;1-119/Domain: pre-S1 domain #status predicted <PRE1>
F;120-400/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <P
F;120-174/Domain: pre-S2 domain #status predicted <PRE2>
F;175-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 52.7%; Score 39; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 SKLMSGGLNISEPN 15
Db 6 SKPRKGMGTLSVNP 20
RESULT 15
SAVLEK
large surface antigen - hepatitis B virus (subtype adw, strain 991)
N;Contains: major surface antigen; middle surface antigen
C;Species: hepatitis B virus, HBV
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S10383
R;Koehel, H.G.; Schueler, A.; Lottmann, S.; Thomsen, R.
submitted to the EMBL Data Library, February 1990
A;Reference number: S10380
A;Accession: S10383
A;Molecule type: DNA
A;Residues: 1-400 <KOE>
A;Cross-references: UNIPROT:P17101; UNIPARC:UPI00001389B8; EMBL:X51970; NID:g115012; PI
C;Genetics:
A;Gene: pre-S1/pre-S2/S
A;Introns: 123/2
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;120-400/Product: middle surface antigen (gene S) #status predicted <MSA>
F;175-400/Product: major surface antigen (gene S) #status predicted <MSA>
F;115,123,177/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 52.7%; Score 39; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 SKLMSGGLNISEPN 15
Db 6 SKPRKGMGTLSVNP 20
Search completed: June 13, 2006, 04:20:33
Job time : 16.2206 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:58:38 ; Search time 121.103 Seconds
(without alignments)
114.574 Million cell updates/sec

Title: US-10-612-162A-3
Perfect score: 74
Sequence: 1 SKLSMGSGLNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	1 TRFE_HUMAN	P02787 homo sapien
2	60	81.1	698	2 Q53H26_HUMAN	Q53H26 homo sapien
3	48	64.9	697	2 Q5R9L7_PONPY	Q5R9L7 pongo pygma
4	47	63.5	400	2 Q9E952_HBV	Q9E952 hepatitis b
5	47	63.5	521	2 Q943K6_ORYSA	Q943K6 oryza sativ
6	46	62.2	823	2 Q5A1Q2_CANAL	Q5A1Q2 candida alb
7	46	62.2	823	2 Q8U2T2_CANAL	Q8U2T2 candida alb
8	45	60.8	347	2 Q45RA5_STRFR	Q45RA5 streptomyc
9	45	60.8	444	2 Q3YJ25_HAEPR	Q3YJ25 haemophilus
10	45	60.8	694	2 Q5BE11_EMENT	Q5BE11 emment
11	45	60.8	3008	2 Q5CSS5_CRYPV	Q5CSS5 cryptospori
12	44	59.5	894	2 Q4SON4_TETNG	Q4SON4 tetradon n
13	43	58.1	100	2 Q59NH2_CANAL	Q59NH2 candida alb
14	43	58.1	341	1 PEXL1_BRARE	PEXL1 brachydanio
15	43	58.1	796	2 Q8NC87_HUMAN	Q8NC87 homo sapien
16	43	58.1	1972	1 BAZ289_HUMAN	Q8NC87 homo sapien
17	43	58.1	3608	2 Q5TOJ2_ANOGA	Q5TOJ2 anopheles g
18	42.5	57.4	994	2 Q43GK1_3CHLB	Q43GK1 chlorobium
19	42	56.8	307	2 Q6FMK0_CANCA	Q6FMK0 candida gla
20	42	56.8	376	2 Q2UC93_ASFOR	Q2UC93 aspergillus
21	42	56.8	428	2 Q8GP40_STRTR	Q8GP40 streptococ
22	42	56.8	528	2 Q8J289_KLULA	Q8J289 kluyveromyc
23	42	56.8	698	2 Q4R5M1_MACFA	Q4R5M1 macaca fasc
24	42	56.8	867	2 Q8U379_PYRFU	Q8U379 pyrococcus
25	42	56.8	1053	2 Q5CPH7_CRYPV	Q5CPH7 cryptospori
26	41	55.4	145	2 Q3YI09_SHISS	Q3YI09 shigelia so
27	41	55.4	148	1 YGEF_ECOLI	Q46786 escherichia
28	41	55.4	148	2 Q2M9Y7_ECOLI	Q2M9Y7 escherichia
29	41	55.4	148	2 Q9D019_MOUSE	Q9D019 mus musculu
30	41	55.4	163	2 Q8X6H8_ECO57	Q8X6H8 escherichia
31	41	55.4	174	2 Q8V4P7_HBV	Q8V4P7 hepatitis b

ALIGNMENTS

RESULT 1	TRFE_HUMAN	STANDARD;	PRT;	698 AA.
ID	P02787; Q43890; Q9NOB8; Q9UHV0;			
AC	21-JUL-1986, integrated into UniProtKB/Swiss-Prot.			
DT	01-OCT-1989, sequence version 2.			
DT	07-MAR-2006, entry version 84.			
DE	Serotransferrin precursor (Transferrin) (Beta-1-metal-binding globulin).			
GN	Name=TF; ORFNames=PRO1400;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE. AND VARIANTS TF*B2; TF*CH1 AND TF*DI.			
RX	MEDLINE=84194084; PubMed=6585826;			
RA	Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,			
RA	van Bragt P.H., Baldwin W.D., Bowman B.H.;			
RT	"Human transferrin: cDNA characterization and chromosomal localization.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;			
RA	Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,			
RA	Chambon P., Cohen G.N., Zakim M.M.;			
RT	"Complete structure of the human transferrin gene. Comparison with analogous chicken gene and human pseudogene.";			
RL	Gene 56:109-116(1987).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Liver;			
RX	MEDLINE=92213399; PubMed=1809186;			
RA	Hershenberger C.L., Larson J.L., Arnold B., Rosebeck P.R. Jr.,			
RA	Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemann M.W., Tice P.A.;			
RT	"A cloned gene for human transferrin.";			
RL	Ann. N. Y. Acad. Sci. 646:140-154(1991).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE. AND VARIANT ATRANSFERRINEMIA PRO-477.			
RX	MEDLINE=20563920; PubMed=1110675;			
RA	Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,			
RA	Fairbanks V.P.;			
RT	"Molecular characterization of a case of atransferrinemia.";			
RL	Blood 96:4071-4074(2000).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RA	Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,			
RA	Altearn M.O., Kuldaneck S.A., Rajkumar N., Toth E.J., Yi Q.,			
RA	Nickerson D.A.;			
RT	"SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			

32	41	55.4	174	2 Q8V4Q0_HBV	Q8V4Q0 hepatitis b
33	41	55.4	234	2 Q647Z6_3ARCH	Q647Z6 uncultured
34	41	55.4	253	2 Q6BCP0_HBV	Q6BCP0 hepatitis b
35	41	55.4	400	2 Q7TDQ3_HBV	Q7TDQ3 hepatitis b
36	41	55.4	400	2 Q9Q3F5_HBV	Q9Q3F5 hepatitis b
37	41	55.4	491	2 Q5V5I8_HALMA	Q5V5I8 haloarcula
38	41	55.4	584	2 Q5B2X0_EMENT	Q5B2X0 aspergillus
39	41	55.4	587	2 Q2KCN2_LISWE	Q2KCN2 listeria we
40	41	55.4	722	1 CM007_MOUSE	Q8K2Y0 mus musculu
41	41	55.4	1257	2 Q5ALV2_CANAL	Q5ALV2 candida alb
42	41	55.4	1433	2 Q8A043_BACTN	Q8A043 bacteroides
43	41	55.4	1482	1 CFTF_CARPS	Q2GLC5 carollia pe
44	40	54.1	92	2 Q80B33_HBV	Q80B33 hepatitis b
45	40	54.1	97	2 Q80B32_HBV	Q80B32 hepatitis b

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stupieniewski M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosak S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bask S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [17]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 99-698.
 RC TISSUE=Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.,
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [18]
 RP NUCLEOTIDE SEQUENCE OF 422-698.
 RX MEDLINE=84153910; PubMed=6322780;
 RA Uzan G., Fraim M., Park I., Besmond C., Maessen G., Trepac J.S.,
 RA Zakin M.M., Kahn A.,
 RT "Molecular cloning and sequence analysis of cDNA for human
 RT transferrin.";
 RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
 RN [19]
 RP PROTEIN SEQUENCE OF 20-698.
 RX MEDLINE=83160878; PubMed=6833213;
 RA MCGILLIVRAY R.T.A., Mendez E., Shevale J.G., Sinha S.K.,
 RA Lineback-Zins J., Brew K.,
 RT "The primary structure of human serum transferrin. The structures of
 RT seven cyanogen bromide fragments and the assembly of the complete
 RT structure.";
 RL J. Biol. Chem. 258:3543-3553(1983).
 RN [10]
 RP NUCLEOTIDE SEQUENCE OF 73-698.
 RX MEDLINE=85216459; PubMed=385812;
 RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
 RA Zakin M.M.,
 RT "Organization of the human transferrin gene: direct evidence that it
 RT originated by gene duplication.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 1-14.
 RX MEDLINE=87066744; PubMed=3786138;
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.,
 RT "The 5' region of the human transferrin gene: structure and potential
 RT regulatory sites.";
 RL Nucleic Acids Res. 14:8692-8692(1986).
 RN [12]
 RP NUCLEOTIDE SEQUENCE OF 1-72 AND 291-300.
 RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
 RA Adrian G.S., Kiriak B.W., Bowman B.H., Yang F.,
 RT "The human transferrin gene: 5' region contains conserved sequences
 RT which match the control elements regulated by heavy metals,
 RT glucocorticoids and acute phase reaction.";
 RL Gene 49:167-175(1986).
 RN [13]
 RP NUCLEOTIDE SEQUENCE OF 45-72.
 RX MEDLINE=20392111; PubMed=10931525;
 RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
 RA Bepinos de los Monteros A., de Vellos J., Zakin M.M., Baron B.,
 RT "Alternative splicing prevents transferrin secretion during
 RT differentiation of a human oligodendrocyte cell line.";
 RL J. Neurosci. Res. 61:388-395(2000).
 RN [14]
 RP NUCLEOTIDE SEQUENCE OF 564-624, AND VARIANT TP+C2.
 RC TISSUE=Brain;
 RX MEDLINE=97418135; PubMed=9272172; DOI=10.1007/s004390050533;
 RA Nemekeka K., Oyama F., Imagawa M., Ihara Y.,
 RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
 RT C1 or Tf C2 variant.";
 RL Hum. Genet. 100:457-458(1997).
 RN [15]
 RP NUCLEOTIDE SEQUENCE OF 564-624.
 RA Tsuchida S., Ikemoto S., Kajii E.,
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP NUCLEOTIDE SEQUENCE OF 636-696.
 RX MEDLINE=89386721; PubMed=2780570;
 RA Duguid J.R., Bohmont C.W., Liu N.G., Tourtellotte W.W.,
 RT "Changes in brain gene expression shared by scrapie and Alzheimer
 RT disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
 RN [17]
 RP PROTEIN SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Ershova E.S., Egorov T.A., Musalyanov A.K.,
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [18]
 RP DISULFIDE BONDS.
 RX MEDLINE=82222166; PubMed=6953407;
 RA MCGILLIVRAY R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
 RA Lineback-Zins J., Brew K.,
 RT "The complete amino acid sequence of human serum transferrin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
 RN [19]
 RP MUTAGENESIS.
 RX MEDLINE=92031536; PubMed=1932003;
 RA Woodworth R.C., Mason A.B., Funk W.D., MCGILLIVRAY R.T.A.,
 RT "Expression and initial characterization of five site-directed mutants
 RT of the N-terminal half-molecule of human transferrin.";
 RL Biochemistry 30:10824-10829(1991).
 RN [20]
 RP CARBOHYDRATE-LINKAGE SITES ASN-432 AND ASN-630.
 RX PubMed=16335952; DOI=10.1021/pr0502065;
 RA Liu T., Qian W.-J., Grilcenko M.A., Camp D.G. II, Monroe M.E.,
 RA Moore R.J., Smith R.D.,
 RT "Human plasma N-glycoproteome analysis by immunofluorescence subtraction,
 RT hydrazide chemistry, and mass spectrometry.";
 RL J. Proteome Res. 4:2070-2080(2005).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
 RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/bi9803551;
 RA MCGILLIVRAY R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
 RA Woodworth R.C., Brayer G.D., Baker E.N.,
 RT "Two high-resolution crystal structures of the recombinant N-lobe of
 RT human transferrin reveal a structural change implicated in iron
 RT release.";
 RL Biochemistry 37:7919-7928(1998).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
 RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/bi9812064;
 RA Jeffery P.D., Bewley M.C., MCGILLIVRAY R.T.A., Mason A.B.,
 RA Woodworth R.C., Baker E.N.,

RT "ligand-induced conformational change in transferrins: crystal
RT structure of the open form of the N-terminal half-molecule of human
Query Match 81.1%; Score 60; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.09;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLEPN 15
DB 515 KLCWGSGLNLEPN 528
RESULT 2
Q53H26_HUMAN PRELIMINARY; PRT; 698 AA.
AC Q53H26;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Transferrin variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94117032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL AK222755; BAD96475.1; -; mRNA.
DR SMR; Q53H26; 23-346.
DR Ensembl; ENSG00000091513; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferriic iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
FT NON_TER 1
SQ SEQUENCE 698 AA; 77080 MW; A54775D23B9A4FFP CRC64;
Query Match 81.1%; Score 60; DB 2; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.09;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLEPN 15
DB 515 KLCWGSGLNLEPN 528
RESULT 3
Q5R9L7_PONPY PRELIMINARY; PRT; 697 AA.
AC Q5R9L7;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein DKFZP459H0229.
GN Name=DKFZP459H0229;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Pongo.
NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osenger A., Fobz G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL CR859370; CAH91543.1; -; mRNA.
DR SMR; Q5R9L7; 23-346.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferriic iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
DR Hypothetical protein.
SQ SEQUENCE 697 AA; 77010 MW; 3567442528B42833 CRC64;
Query Match 64.9%; Score 48; DB 2; Length 697;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLEPN 15
DB 514 KLCWGSGLNLEPN 527
RESULT 4
Q9E952_HBV PRELIMINARY; PRT; 400 AA.
AC Q9E952;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Large surface antigen.
OS Hepatitis B virus (HBV).
OC Viruses; Retro-transcribing viruses; Hepadnaviridae;
OC Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20528423; PubMed=11074474;
DOI=10.1002/1096-9071(200012)62:4<456::AID-JMV10>3.0.CO;2-3;
RA Suganuchi F., Mizokami M., Orito E., Ohno T., Kato H., Maki M.,


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OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Emericella.
OX NCBI_TaxId=227321;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=FGSC 4;
RX PubMed=16372000; DOI=10.1038/nature04341;
RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA Batzoglou S., Lee S.-I., Bastenkmann M., Spevak C.C., Clutterbuck J.,
RA Kapitonov V., Jurka J., Scaccocchio C., Farman M., Butler J.,
RA Purcell S., Harris S., Bruns G.H., Drah O., Busch S., D'Elfert C.,
RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA Doonan J.H., Yu J., Venken K., Pain A., Freitag M., Selker E.U.,
RA Archer D.B., Penhaly M.A., Oakley B.R., Momany M., Tanaka T.,
RA Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
RA Caddick M., Hynes M., Pacletti M., Fischer R., Miller B.L., Dyer P.S.,
RA Sachs M.S., Osmani S.A., Birren B.W.;
RT "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT fumigatus and A. oryzae."
RL Nature 438:1105-1115(2005).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL; AACD0100017; EAA65812.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 694 AA; 75941 MW; 70F4501B8C27C083 CRC64;

Query Match 60.8%; Score 45; DB 2; Length 694;
Best Local Similarity 57.1%; Pred. NO. 53;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKLMSGGLNLSEPP 14
DB 342 SNLSTGSGASWSQP 355

RESULT 11
OS CRYPTOPARV PRELIMINARY; PRT; 3008 AA.
AC Q5C8S5;
ID 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DY 07-FEB-2006, entry version 5.
DE Extracellular membrane associated protein with a signal peptide, EGF
DE domain, 9x transmembrane domains and a pentraxin domain.
GN ORFNames=cgcl_1520;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporididae; Cryptosporidium.
OX NCBI_TaxId=5807;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
RA Lancelo C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum."
RL Science 304:441-445(2004).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC

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DR EMBL; AAEE01000006; EAK88440.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IBA.
DR InterPro; IPR013320; Com_1like_subgrp.
KM Repeat; Transmembrane.
SQ SEQUENCE 3008 AA; 343678 MW; F09C5C3ED972011C CRC64;

Query Match 60.8%; Score 45; DB 2; Length 3008;
Best Local Similarity 64.3%; Pred. NO. 3e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMSGGLNLSEPP 15
DB 1032 KLMRGGLLSEPPN 1045

RESULT 12
OS Q4SON4_TETNG PRELIMINARY; PRT; 894 AA.
ID Q4SON4_TETNG
AC Q4SON4;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DY 07-FEB-2006, sequence version 1.
DE Chromosome 17 SCAP14532, whole genome shotgun sequence.
GN ORFNames=GSTENG00014297001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Vallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulin J., De Bernardis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RP GenomeScope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
-----
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CC
DR EMBL; CAEE01014532; CAF97048.1; -; Genomic DNA.
SQ SEQUENCE 894 AA; 99528 MW; B7B8544F5F21784 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 894;
Best Local Similarity 64.3%; Pred. NO. 1.1e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SKLMSGGLNLSEPP 14
DB 587 SKTSVSGSLSEPP 600

RESULT 13
Q59NH2_CANAL

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ID 059NH2_CANAL PRELIMINARY; PRT; 100 AA.
AC 059NH2;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN ORFNames=Ca019.11674, Ca019.4198;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federapief N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAC001000206; EAK92015.1; -; Genomic DNA.
DR EMBL; AAC001000205; EAK92038.1; -; Genomic DNA.
KM Hypothetical protein.
SQ SEQUENCE 100 AA; 10879 MW; C3B55B7D712665F CRC64;

Query Match 58.1%; Score 43; DB 2; Length 100;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSGSGLNSEPN 15
Db 61 KLSIDSSANLSNPN 74

RESULT 14
PDK1L_BRARE STANDARD; PRT; 341 AA.
ID PDK1L_BRARE
AC Q32P93;
DT 24-JAN-2006, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2005, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE Serine/threonine-protein kinase pdk1l (EC 2.7.1.37).
GN Name=pdk1l; ORFNames=zgc:123209;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Ovary;
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Nucleus (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Glu-37 is present instead of the conserved Lys which is
CC expected to be an active site residue. Lys-38 may fulfill that
CC role.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; BC108040; AA108041.1; -; mRNA.
DR ZFIN; ZDB-GENE-051133-236; zgc:123209.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

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DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT CHAIN 1 341
FT DOMAIN 8 332 Protein kinase.
FT NP_BIND 14 22 ATP (By similarity).
FT ACT_SITE 164 164 Proton acceptor (By similarity).
SQ SEQUENCE 341 AA; 38205 MW; 40318BD00BEF0778 CRC64;

Query Match 58.1%; Score 43; DB 1; Length 341;
Best Local Similarity 64.3%; Pred. No. 55;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SKLSGSGLNSEPN 14
Db 194 SKVSGSGLNSEPN 207

RESULT 15
ID 08NC87_HUMAN PRELIMINARY; PRT; 796 AA.
AC 08NC87;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 21-FEB-2006, entry version 17.
DE CDNA FLJ90414 f1s, clone NT2RP3000125, similar to RETINOBLASTOMA
DE BINDING PROTEIN 2. (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Iisogai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hito Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuma S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nishimura K.;
RL "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK074895; BAC11274.1; -; mRNA.
DR HSSP; Q9UIG0; 1f62.
DR Ensemble; ENSG00000123636; Homo sapiens.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SMO0249; PHD; 1.
DR PROSITE; PS50016; ZF_PHD_2; 1.
FT NON_TER 796
SQ SEQUENCE 796 AA; 88463 MW; 2EDB8BCAF9720C1E CRC64;

Query Match 58.1%; Score 43; DB 2; Length 796;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SMGSGLNSEPN 15
Db 416 SLGSGLNSEGN 427

Search completed: June 13, 2006, 04:17:49
Job time : 124.103 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:20:54 ; Search time 26.4706 Seconds
(without alignments)
49.601 Million cell updates/sec

Title: US-10-612-162A-3
Perfect score: 74
Sequence: 1 SKLMSGSLNLSPPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues
Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCTUS.COMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	1	US-08-175-158A-2
2	60	81.1	698	2	US-09-439-740-2
3	60	81.1	1074	1	US-08-470-058-2
4	60	81.1	1074	2	US-09-037-188-2
5	60	81.1	1074	2	US-09-285-310-2
6	60	81.1	1074	2	US-09-753-385-2
7	60	81.1	1410	1	US-08-470-058-4
8	60	81.1	1410	2	US-09-037-188-4
9	60	81.1	1410	2	US-09-285-310-4
10	60	81.1	1410	2	US-09-753-385-4
11	52	70.3	439	7	5262177-4
12	46	62.2	439	2	US-09-248-796A-15968
13	46	58.1	1969	2	US-09-418-710-72
14	43	58.1	1969	2	US-09-839-479-71
15	43	58.1	1972	2	US-09-418-710-21
16	43	58.1	1972	2	US-09-839-479-21
17	41	55.4	148	2	US-09-711-164-464
18	41	55.4	884	2	US-09-248-796A-20574
19	40.5	54.7	504	2	US-09-488-039A-11966
20	40	54.1	125	2	US-08-480-173A-50
21	40	54.1	125	2	US-08-484-408A-50
22	40	54.1	170	1	US-08-683-262B-49
23	40	54.1	170	2	US-09-361-707-49
24	40	54.1	174	1	US-08-683-262B-38
25	40	54.1	174	1	US-08-683-262B-39
26	40	54.1	174	1	US-08-683-262B-42

27	40	54.1	174	1	US-08-683-262B-43	Sequence 43, Appl
28	40	54.1	174	1	US-08-683-262B-44	Sequence 44, Appl
29	40	54.1	174	1	US-08-683-262B-45	Sequence 45, Appl
30	40	54.1	174	1	US-08-683-262B-46	Sequence 46, Appl
31	40	54.1	174	1	US-08-683-262B-47	Sequence 47, Appl
32	40	54.1	174	1	US-08-683-262B-48	Sequence 48, Appl
33	40	54.1	174	2	US-08-480-173A-48	Sequence 48, Appl
34	40	54.1	174	2	US-08-484-408A-48	Sequence 48, Appl
35	40	54.1	174	2	US-09-361-707-38	Sequence 48, Appl
36	40	54.1	174	2	US-09-361-707-39	Sequence 48, Appl
37	40	54.1	174	2	US-09-361-707-42	Sequence 42, Appl
38	40	54.1	174	2	US-09-361-707-43	Sequence 44, Appl
39	40	54.1	174	2	US-09-361-707-44	Sequence 45, Appl
40	40	54.1	174	2	US-09-361-707-45	Sequence 46, Appl
41	40	54.1	174	2	US-09-361-707-46	Sequence 47, Appl
42	40	54.1	174	2	US-09-361-707-47	Sequence 48, Appl
43	40	54.1	174	2	US-09-361-707-48	Sequence 48, Appl
44	40	54.1	174	7	5204096-5	Patent No. 5204096
45	40	54.1	358	2	US-09-328-352-7579	Sequence 7579, Ap

ALIGNMENTS

RESULT 1
US-08-175-158A-2
Sequence 2, Application US/08175158A
Patent No. 5986067
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MACGILLIVRAY, Rose T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODMORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,158A
FILING DATE: 28-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,029
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-0050CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-175-158A-2
Query Match 81.1%; Score 60; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.022;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNISEPN 15
DB 515 KLCMGSGNLNCEPN 528

RESULT 2

US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MacGILLIVRAY, Ross T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRIN HALF-
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match 81.1%; Score 60; DB 2; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.022;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNISEPN 15
DB 515 KLCMGSGNLNCEPN 528

RESULT 3
US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 81.1%; Score 60; DB 1; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.036;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNISEPN 15
DB 891 KLCMGSGNLNCEPN 904

RESULT 4
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 81.1%; Score 60; DB 2; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.036;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 891 KLCWGSGLNLEPN 904

RESULT 5

US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
City: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 81.1%; Score 60; DB 2; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.036;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 891 KLCWGSGLNLEPN 904

RESULT 6
US-09-753-385-2
Sequence 2, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
TITLE OF INVENTION: OF A SELECTED SUBSTANCE INTO CELLS
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1074
TYPE: PRT
ORGANISM: Homo sapiens
US-09-753-385-2

Query Match 81.1%; Score 60; DB 2; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.036;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 891 KLCWGSGLNLEPN 904

RESULT 7

US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
City: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 81.1%; Score 60; DB 1; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 1227 KLCMSSGLNLCEPN 1240

RESULT 8
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 81.1%; Score 60; DB 2; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 1227 KLCMSSGLNLCEPN 1240

RESULT 9
US-09-285-310-4
Sequence 4, Application US/09285310

Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 81.1%; Score 60; DB 2; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 1227 KLCMSSGLNLCEPN 1240

RESULT 10
US-09-753-385-4
Sequence 4, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
TITLE OF INVENTION: OF A SELECTED SUBSTANCE INTO CELLS
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4

LENGTH: 1410
TYPE: PRT
ORGANISM: Homo sapiens
US-09-753-385-4

Query Match 81.1%; Score 60; DB 2; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNSEPN 15
Db 1227 KLCMSGSLNCEPN 1240

RESULT 11
5262177-4
PATENT NO. 5262177
APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGGERD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO: 4
LENGTH: 696
5262177-4

Query Match 70.3%; Score 52; DB 7; Length 696;
Best Local Similarity 78.6%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMSGSLNSEPN 15
Db 514 KLCMSGSLNCEPN 527

RESULT 12
US-09-248-796A-15968
SEQUENCE 15968, Application US/09248796A
PATENT NO. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15968
LENGTH: 439
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (12)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-15968

Query Match 62.2%; Score 46; DB 2; Length 439;
Best Local Similarity 57.1%; Pred. No. 4.5;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKLSMSGSLNSEPN 14

Db 351 SPMSMGAGINWTER 364

RESULT 13
US-09-418-710-72
SEQUENCE 72, Application US/09418710
PATENT NO. 6596482
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 1969
TYPE: PRT
ORGANISM: Homo sapiens
US-09-418-710-72

Query Match 58.1%; Score 43; DB 2; Length 1969;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SMGSGSLNSEPN 15
Db 1454 SLGSGSLNSEGN 1465

RESULT 14
US-09-839-479-71
SEQUENCE 71, Application US/09839479
PATENT NO. 6727222
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 1969
TYPE: PRT
ORGANISM: Homo sapiens
US-09-839-479-71

Query Match 58.1%; Score 43; DB 2; Length 1969;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SMGSGSLNSEPN 15
Db 1454 SLGSGSLNSEGN 1465

RESULT 15

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US-09-418-710-21
; Sequence 21, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418, 710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-21

Query Match      58.1%; Score 43; DB 2; Length 1972;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 SMGSGJNLSEPN 15
      |:||||| |||
Db      1457 SLGSGJLSEGN 1468
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Search completed: June 13, 2006, 04:25:49
Job time : 27.4706 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:24 ; Search time 86.25 Seconds
(without alignments)
80.559 Million cell updates/sec

Title: US-10-612-162a-3
Sequence: 1 SKLMSGGLNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US10_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/pcodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	US-10-612-162-3	Sequence 3, Appli
2	60	81.1	42	US-10-378-094-15	Sequence 15, Appli
3	60	81.1	42	US-10-384-060-36	Sequence 36, Appli
4	60	81.1	328	US-09-891-126-5	Sequence 5, Appli
5	60	81.1	328	US-10-266-745-5	Sequence 5, Appli
6	60	81.1	679	US-10-378-094-3	Sequence 3, Appli
7	60	81.1	679	US-10-384-060-3	Sequence 3, Appli
8	60	81.1	679	US-10-231-484-3	Sequence 3, Appli
9	60	81.1	679	US-10-429-482-4	Sequence 4, Appli
10	60	81.1	679	US-10-429-497-4	Sequence 4, Appli
11	60	81.1	679	US-10-429-515-4	Sequence 4, Appli
12	60	81.1	679	US-10-429-598-4	Sequence 4, Appli
13	60	81.1	679	US-10-429-635-4	Sequence 4, Appli
14	60	81.1	679	US-10-429-653-4	Sequence 4, Appli
15	60	81.1	679	US-10-429-659-4	Sequence 4, Appli
16	60	81.1	679	US-10-429-661-4	Sequence 4, Appli
17	60	81.1	679	US-10-429-660-4	Sequence 4, Appli
18	60	81.1	679	US-10-429-662-4	Sequence 4, Appli
19	60	81.1	679	US-10-429-655-4	Sequence 4, Appli
20	60	81.1	679	US-10-429-654-4	Sequence 4, Appli
21	60	81.1	698	US-09-935-642-6	Sequence 6, Appli
22	60	81.1	698	US-10-378-094-2	Sequence 2, Appli
23	60	81.1	698	US-10-384-060-2	Sequence 2, Appli
24	60	81.1	698	US-10-231-494-2	Sequence 2, Appli
25	60	81.1	698	US-10-383-201-10	Sequence 10, Appli
26	60	81.1	698	US-10-383-201-14	Sequence 14, Appli
27	60	81.1	698	US-10-887-711-2	Sequence 2, Appli

28	60	81.1	698	US-10-513-523-3	Sequence 3, Appli
29	60	81.1	698	US-11-177-506-46	Sequence 46, Appli
30	60	81.1	698	US-11-038-901-2	Sequence 2, Appli
31	60	81.1	1074	US-09-753-385-2	Sequence 2, Appli
32	60	81.1	1410	US-09-753-385-4	Sequence 4, Appli
33	60	81.1	1418	US-10-473-127-804	Sequence 804, App
34	57	77.0	1410	US-10-473-127-805	Sequence 805, App
35	55	74.3	15	US-10-769-514-10	Sequence 10, Appli
36	55	74.3	15	US-10-769-514-42	Sequence 42, Appli
37	55	74.3	15	US-10-801-990-180	Sequence 180, App
38	55	74.3	15	US-10-801-990-184	Sequence 184, App
39	55	74.3	26	US-10-801-990-14	Sequence 14, Appli
40	47	63.5	340	US-10-437-963-110132	Sequence 110132, A
41	43	58.1	91	US-09-864-761-36754	Sequence 36754, A
42	43	58.1	1969	US-09-839-479-71	Sequence 71, Appli
43	43	58.1	1969	US-10-376-537-72	Sequence 72, Appli
44	43	58.1	1969	US-10-702-148-71	Sequence 71, Appli
45	43	58.1	1972	US-09-839-479-21	Sequence 21, Appli

ALIGNMENTS

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RESULT 1
US-10-612-162-3
; Sequence 3, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; TITLE OF INVENTION: antibodies, their preparation and use
; FILE REFERENCE: 2002/B001
; CURRENT FILING DATE: US/10/612.162
; PRIOR APPLICATION NUMBER: 2003-07-03
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-612-162-3

Query Match      100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SKLMSGGLNLSEPN 15
Db      1 SKLMSGGLNLSEPN 15

RESULT 2
US-10-378-094-15
; Sequence 15, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378.094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231.494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
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;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 15
;; LENGTH: 42
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: C1 subdomain of transferrin
US-10-378-094-15

Query Match 81.1%; Score 60; DB 4; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0036;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNISEPN 15
Db 25 KLCMSGSLNICEPN 38

RESULT 3
US-10-384-060-36
;; Sequence 36, Application US/10384060
;; Publication No. US20030226155A1
;; GENERAL INFORMATION:
;; APPLICANT: SADEGHI, Homayoun
;; APPLICANT: PRIOR, Christopher P.
;; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
;; FILE REFERENCE: 54710-5004-US
;; CURRENT APPLICATION NUMBER: US/10/384,060
;; PRIOR FILING DATE: 2003-03-10
;; PRIOR APPLICATION NUMBER: US 10/231,494
;; PRIOR FILING DATE: 2002-08-30
;; PRIOR APPLICATION NUMBER: US 60/334,059
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: US 60/315,745
;; PRIOR FILING DATE: 2001-08-30
;; PRIOR APPLICATION NUMBER: US 60/406,977
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 36
;; LENGTH: 42
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: C1 domain of human Tf
US-10-384-060-36

Query Match 81.1%; Score 60; DB 4; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0036;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNISEPN 15
Db 25 KLCMSGSLNICEPN 38

RESULT 4
US-09-891-126-5
;; Sequence 5, Application US/09891126
;; Patent No. US20020072596A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
;; FILE REFERENCE: PT035P1
;; CURRENT APPLICATION NUMBER: US/09/891,126
;; PRIOR FILING DATE: 2001-06-26
;; PRIOR APPLICATION NUMBER: PCT/US00/34769
;; PRIOR FILING DATE: 2000-12-21
;; PRIOR APPLICATION NUMBER: 60/171,595

;; PRIOR FILING DATE: 1999-12-23
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 328
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-891-126-5

Query Match 81.1%; Score 60; DB 3; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.035;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNISEPN 15
Db 179 KLCMSGSLNICEPN 192

RESULT 5
US-10-266-745-5
;; Sequence 5, Application US/10266745
;; Publication No. US20030149256A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
;; FILE REFERENCE: PT035P1
;; CURRENT APPLICATION NUMBER: US/10/266,745
;; PRIOR FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: US/09/891,126
;; PRIOR FILING DATE: 2001-06-26
;; PRIOR APPLICATION NUMBER: PCT/US00/34769
;; PRIOR FILING DATE: 2000-12-21
;; PRIOR APPLICATION NUMBER: 60/171,595
;; PRIOR FILING DATE: 1999-12-23
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 328
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-266-745-5

Query Match 81.1%; Score 60; DB 4; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.035;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMSGSLNISEPN 15
Db 179 KLCMSGSLNICEPN 192

RESULT 6
US-10-378-094-3
;; Sequence 3, Application US/10378094
;; Publication No. US20030221201A1
;; GENERAL INFORMATION:
;; APPLICANT: PRIOR, Christopher P.
;; APPLICANT: LAI, Char-Huei
;; APPLICANT: SADEGHI, Homayoun
;; APPLICANT: TURNER, Andrew
;; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
;; FILE REFERENCE: 54710-5001-01-US
;; CURRENT APPLICATION NUMBER: US/10/378,094
;; PRIOR FILING DATE: 2003-03-04
;; PRIOR APPLICATION NUMBER: US 10/231,494
;; PRIOR FILING DATE: 2002-08-30
;; PRIOR APPLICATION NUMBER: US 60/334,059
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: US 60/315,745
;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 3

LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3

Query Match 81.1%; Score 60; DB 4; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 496 KLCWGSGLNLEPN 509

RESULT 7
US-10-384-060-3
Sequence 3, Application US/10384060
Publication No. US2003026155A1
GENERAL INFORMATION:
APPLICANT: SADEGHI, Homayoun
APPLICANT: TURNER, Andrew
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-US
CURRENT APPLICATION NUMBER: US/10/384,060
CURRENT FILING DATE: 2003-03-10
PRIORITY APPLICATION NUMBER: US 10/231,494
PRIORITY FILING DATE: 2002-08-30
PRIORITY APPLICATION NUMBER: US 60/334,059
PRIORITY FILING DATE: 2001-11-30
PRIORITY APPLICATION NUMBER: US 60/315,745
PRIORITY FILING DATE: 2001-08-30
PRIORITY APPLICATION NUMBER: US 60/406,977
PRIORITY FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match 81.1%; Score 60; DB 4; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 496 KLCWGSGLNLEPN 509

RESULT 8
US-10-231-494-3
Sequence 3, Application US/10231494
Publication No. US2004002334A1
GENERAL INFORMATION:
APPLICANT: PILOT, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIORITY APPLICATION NUMBER: US 60/315,745
PRIORITY FILING DATE: 2001-08-30
PRIORITY APPLICATION NUMBER: US 60/334,059
PRIORITY FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3

Query Match 81.1%; Score 60; DB 4; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 496 KLCWGSGLNLEPN 509

RESULT 9
US-10-429-482-4
Sequence 4, Application US/10429482
Publication No. US20040219097A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tumors
FILE REFERENCE: 2537,000001
CURRENT APPLICATION NUMBER: US/10/429,482
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-482-4

Query Match 81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 496 KLCWGSGLNLEPN 509

RESULT 10
US-10-429-497-4
Sequence 4, Application US/10429497
Publication No. US20040219098A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Methods For The Treatment of Tumors
FILE REFERENCE: 2537,000006
CURRENT APPLICATION NUMBER: US/10/429,497
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-497-4

Query Match 81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEPN 15
DB 496 KLCWGSGLNLEPN 509

RESULT 11
US-10-429-515-4

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; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537.000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4
```

```
Query Match      81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMGSGLNISEPN 15
DB      496 KLCMGSGLNICEPN 509
```

```
RESULT 12
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment Of Tumors
; FILE REFERENCE: 2537.000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4
```

```
Query Match      81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMGSGLNISEPN 15
DB      496 KLCMGSGLNICEPN 509
```

```
RESULT 13
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537.000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4
```

```
Query Match      81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 KLSMGSGLNISEPN 15
DB      496 KLCMGSGLNICEPN 509
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RESULT 14
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4
```

```
Query Match      81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMGSGLNISEPN 15
DB      496 KLCMGSGLNICEPN 509
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```
RESULT 15
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4
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```
Query Match      81.1%; Score 60; DB 5; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.079;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 KLSMGSGLNISEPN 15
DB      496 KLCMGSGLNICEPN 509
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Search completed: June 13, 2006, 04:56:23
Job time : 86.25 secs
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:58 ; Search time 5.07353 Seconds

(Without alignments)
37.380 Million cell updates/sec

Title: US-10-612-162A-3

Sequence: 1 SKLSMSGSLNLEBN 15

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	81.1	679	US-10-515-429-3	Sequence 3, Appli
2	60	81.1	698	US-10-515-429-2	Sequence 2, Appli
3	40	54.1	128	US-10-953-349-18406	Sequence 18406, A
4	40	54.1	167	US-10-953-349-18405	Sequence 18405, A
5	40	54.1	188	US-10-953-349-18404	Sequence 18404, A
6	40	54.1	400	US-11-183-218-46	Sequence 46, Appl
7	40	54.1	409	US-10-953-349-13574	Sequence 13574, A
8	40	54.1	410	US-10-953-349-20639	Sequence 20639, A
9	40	54.1	424	US-10-953-349-13573	Sequence 13573, A
10	40	54.1	425	US-10-953-349-20638	Sequence 20638, A
11	40	54.1	472	US-10-953-349-13572	Sequence 13572, A
12	40	54.1	473	US-10-953-349-20637	Sequence 20637, A
13	39	52.7	290	US-10-471-571A-180	Sequence 180, App
14	38	51.4	208	US-11-293-697-4653	Sequence 4653, Ap
15	38	51.4	275	US-10-953-349-1265	Sequence 1265, Ap
16	38	51.4	599	US-11-293-697-2635	Sequence 2635, Ap
17	37	50.0	271	US-10-953-349-29404	Sequence 29404, A
18	37	50.0	278	US-10-953-349-29403	Sequence 29403, A
19	37	50.0	314	US-10-953-349-29402	Sequence 29402, A
20	35	47.3	198	US-10-953-349-15250	Sequence 15250, A
21	35	47.3	241	US-10-953-349-15249	Sequence 15249, A
22	35	47.3	418	US-10-953-349-13180	Sequence 13180, A
23	35	47.3	440	US-10-953-349-13179	Sequence 13179, A
24	35	47.3	446	US-10-953-349-13178	Sequence 13178, A
25	35	47.3	497	US-10-953-349-13177	Sequence 13177, A

26	35	47.3	511	US-10-953-349-20529	Sequence 20529, A
27	35	47.3	516	US-10-953-349-20528	Sequence 20528, A
28	35	47.3	542	US-10-953-349-20527	Sequence 20527, A
29	35	47.3	706	US-10-505-928-131	Sequence 131, App
30	34	45.9	103	US-10-953-349-20164	Sequence 20164, A
31	34	45.9	138	US-10-953-349-20162	Sequence 20162, A
32	34	45.9	193	US-10-953-349-2812	Sequence 2812, Ap
33	34	45.9	263	US-10-953-349-1332	Sequence 1332, Ap
34	34	45.9	287	US-10-953-349-18594	Sequence 18594, A
35	34	45.9	317	US-10-953-349-18593	Sequence 18593, A
36	34	45.9	344	US-10-953-349-2811	Sequence 2811, Ap
37	34	45.9	358	US-10-953-349-19884	Sequence 19884, A
38	34	45.9	362	US-10-953-349-2810	Sequence 2810, Ap
39	34	45.9	377	US-10-953-349-19883	Sequence 19883, A
40	34	45.9	398	US-10-953-349-19882	Sequence 19882, A
41	34	45.9	444	US-10-953-349-21457	Sequence 21457, A
42	34	45.9	527	US-10-953-349-21456	Sequence 21456, A
43	34	45.9	531	US-10-953-349-21455	Sequence 21455, A
44	34	45.9	743	US-11-293-697-4198	Sequence 4198, Ap
45	33	44.6	73	US-10-488-015-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-515-429-3
Sequence 3, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Mature transferrin protein
US-10-515-429-3
Query Match 81.1%; Score 60; DB 6; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.0048;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 2 KLSMSGSLNLEBN 15
Db 496 KLSMSGSLNLEBN 509
RESULT 2
US-10-515-429-2
Sequence 2, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries

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FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 698
TYPE: PRT
ORGANISM: Homo sapiens
US-10-515-429-2

Query Match      81.1%; Score 60; DB 6; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMGSGLNLSEPN 15
DB      515 KLCMGSGLNLCEPN 528

RESULT 3
US-10-953-349-18406
Sequence 18406, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18406
LENGTH: 128
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-18406

Query Match      54.1%; Score 40; DB 6; Length 128;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 SKLSMGSGLNLSEP 14
DB      24 SKLAVGDGVPSQP 37

RESULT 4
US-10-953-349-18405
Sequence 18405, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18405
LENGTH: 167
TYPE: PRT
ORGANISM: Glycine max

US-10-953-349-18405
Query Match      54.1%; Score 40; DB 6; Length 167;
Best Local Similarity 50.0%; Pred. No. 3.3;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 SKLSMGSGLNLSEP 14
DB      63 SKLAVGDGVPSQP 76

RESULT 5
US-10-953-349-18404
Sequence 18404, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18404
LENGTH: 188
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-18404

Query Match      54.1%; Score 40; DB 6; Length 188;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 SKLSMGSGLNLSEP 14
DB      84 SKLAVGDGVPSQP 97

RESULT 6
US-11-183-218-46
Sequence 46, Application US/11183218
Publication No. US20060088906A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryne
TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
FILE REFERENCE: 040653-01-5083-US02
CURRENT APPLICATION NUMBER: US/11/183,218
CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 10/410,945
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: PCT/US02/32263
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US 60/334,301
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; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/334,233
 ; PRIOR FILING DATE: 2001-11-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 46
 ; LENGTH: 400
 ; TYPE: PRT
 ; ORGANISM: Hepatitis B virus
 ; US-11-183-218-46

Query Match 54.1%; Score 40; DB 7; Length 400;
 Best Local Similarity 60.0%; Pred. No. 8.8;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SKLMSGGLNSEPN 15
 |||
 Db 6 SKPRGGMGTLSVFN 20

RESULT 7
 US-10-953-349-13574
 ; Sequence 13574, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 13574
 ; LENGTH: 409
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-10-953-349-13574

Query Match 54.1%; Score 40; DB 6; Length 409;
 Best Local Similarity 46.2%; Pred. No. 9;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSMGSGGLNSEPN 15
 :|||:
 Db 360 IQLGRGLDIGEPN 372

RESULT 8
 US-10-953-349-20639
 ; Sequence 20639, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 20639
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-10-953-349-20639

Query Match 54.1%; Score 40; DB 6; Length 410;
 Best Local Similarity 46.2%; Pred. No. 9.1;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSMGSGGLNSEPN 15

Db :|||:
 361 IQLGRGLDIGEPN 373

RESULT 9
 US-10-953-349-13573
 ; Sequence 13573, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 13573
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-10-953-349-13573

Query Match 54.1%; Score 40; DB 6; Length 424;
 Best Local Similarity 46.2%; Pred. No. 9.4;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSMGSGGLNSEPN 15
 :|||:
 Db 375 IQLGRGLDIGEPN 387

RESULT 10
 US-10-953-349-20638
 ; Sequence 20638, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 20638
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-10-953-349-20638

Query Match 54.1%; Score 40; DB 6; Length 425;
 Best Local Similarity 46.2%; Pred. No. 9.4;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSMGSGGLNSEPN 15
 :|||:
 Db 376 IQLGRGLDIGEPN 388

RESULT 11
 US-10-953-349-13572
 ; Sequence 13572, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 13572
;
; LENGTH: 472
;
; TYPE: PRT
;
; ORGANISM: Glycine max
;
US-10-953-349-13572

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Query Match	54.1%	Score 40;	DB 6;	Length 472;
Best Local Similarity	46.2%	Pred. No. 11;		
Matches	6;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;

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QY      3  LSMGSGLNISEPN 15
          : : | | : : | |
Db      423  IQLGRGLDIGEPN 435
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RESULT 12
US-10-953-349-20637
/ Sequence 20637, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ TITLE OF INVENTION: ENCODED THERBY
/ FILE REFERENCE: 2/50-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-03-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 20637
/ LENGTH: 473
/ TYPE: PRT
/ ORGANISM: Glycine max
/ US-10-953-349-20637

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Query Match	54.1%	Score 40:	DB 6:	Length 473:
Best Local	Similarity 46.2%	Pred. No. 11:		
Matches 6:	Conservative 4:	Mismatches 3:	Indels 0:	Gaps 0:

QY	3	LSMSGGLNLEPN	15
	:	: : :	
Db	424	IOLGRGLDIGEPN	436

```

RESULT 13
US-10-471-571A-180
; Sequence 180, Application US/10471571A
; Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P02692700
CURRENT APPLICATION NUMBER: US/10/471.571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ. ID NOS: 5642
SOFTWARE: SeqwIn99, version 1.03
; SEQ ID NO 180
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(290)
; OTHER INFORMATION: hypothetical protein
;S-10-471-571A-180

```

Query Match	52.7%;	Score 39;	DB 6;	Length 299;
Best Local Similarity	46.7%;	Pred. No. 9.2;		
Matches	7;	Conservative	5;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	1	SKLSMGSLINSEPN	15	
	:	: : : : : :	:	:

Db 38 AKGTIGSGLRILDPN 52

```

US-11-293-697-4653
RESULT 14
; Sequence 4653, Application US/11293697
; Publication No. US20060105376A1
;
GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4653
; LENGTH: 208
;
TYPE: PR1
;
ORGANISM: Homo sapiens
;
US-11-293-697-4653

```

	Query Match	51.4%;	Score 38;	DB 7;	Length 208;
	Best Local Similarity	72.7%;	Pred. No. 9.4;		
	Matches	8;	Conservative	1;	Mismatches 2; Indels 0; Gaps 0;
QY	4 SMSGINTLSEP	14			
	0				
DG	180 SLGGINTLSEP	190			

```

RESULT 15
US-10-953-349-3265
; Sequence 3265, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3265
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-3265

```

		Query March	51.4%;	Score 38;	DB 6;	Length 275;
		Best Local Similarity	63.6%;	Pred. No. 13;		
		Matches	7;	Conservative	3;	Mismatches
					1;	Indels
					0;	Gaps
QY	2	KLSMGSLNLS	12			
	:	: :				
	db	55	KLPAGACVNLS	65		

Search completed: June 13, 2006, 04:56:53
Job time : 6.07353 secs

CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilizing it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLSMGSGNLSEPN 15
| | | | | | | | | | | | | | |
Db 1 SKLSMGSGNLSEPN 15

RESULT 2

ADRI5909
ID ADRI5909 standard; peptide; 15 AA.

XX
AC ADRI5909;

XX
DT 04-NOV-2004 (first entry)

XX
DE Transferrin peptide fragment #67.

XX
KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX
OS Synthetic.

XX
PN WO2004070389-A1.

XX
PD 19-AUG-2004.

XX
PF 06-FEB-2004; 2004WO-GB000480.

XX
PR 06-FEB-2003; 2003GB-00002740.

XX
PA (AXIS-) AXIS-SHIELD ASA.

XX
PI Rye PD;

XX
DR WPI; 2004-625547/60.

XX
PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.

XX
PS Disclosure; Page 15; 30pp; English.

XX
XX The present invention describes an assay for a protein having at least
XX two isoforms with different glycosylation patterns. The assay involves
XX contacting a sample containing the protein with a proteolytic enzyme,
XX followed by detecting the content or relative content of at least one
XX peptide fragment produced by proteolysis. Also described is a kit for the
XX assay method comprising the proteolytic enzyme and a substrate bound
XX specific binding partner (S1) for at least 2 of the isoforms of the
XX protein. The method can be used for assaying isoforms of proteins
XX according to their glycosylation pattern to determine their concentration
XX or relative concentration in the sample or material (e.g. blood). The
XX method avoids use of antibodies for distinguishing between glycosylated
XX isoforms of the proteins. The present sequence represents a transferrin
XX peptide fragment which is used in the exemplification of the present
XX invention.

XX
SQ Sequence 15 AA;

Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LSWGSGNLSEPN 15
| | | | | | | | | | | | | | |
Db 1 LCMGSGNLCEPN 13

RESULT 3

ADRI5970
ID ADRI5970 standard; peptide; 15 AA.

XX
AC ADRI5970;

XX
DT 04-NOV-2004 (first entry)

XX
DE Transferrin peptide fragment #128.

XX
KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX
OS Synthetic.

XX
PN WO2004070389-A1.

XX
PD 19-AUG-2004.

XX
PF 06-FEB-2004; 2004WO-GB000480.

XX
PR 06-FEB-2003; 2003GB-00002740.

XX
PA (AXIS-) AXIS-SHIELD ASA.

XX
PI Rye PD;

XX
DR WPI; 2004-625547/60.

XX
PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.

XX
PS Disclosure; Page 17; 30pp; English.

XX
XX The present invention describes an assay for a protein having at least
XX two isoforms with different glycosylation patterns. The assay involves
XX contacting a sample containing the protein with a proteolytic enzyme,
XX followed by detecting the content or relative content of at least one
XX peptide fragment produced by proteolysis. Also described is a kit for the
XX assay method comprising the proteolytic enzyme and a substrate bound
XX specific binding partner (S1) for at least 2 of the isoforms of the
XX protein. The method can be used for assaying isoforms of proteins
XX according to their glycosylation pattern to determine their concentration
XX or relative concentration in the sample or material (e.g. blood). The
XX method avoids use of antibodies for distinguishing between glycosylated
XX isoforms of the proteins. The present sequence represents a transferrin
XX peptide fragment which is used in the exemplification of the present
XX invention.

XX
SQ Sequence 15 AA;

Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LSWGSGNLSEPN 15
| | | | | | | | | | | | | | |
Db 1 LCMGSGNLCEPN 13

RESULT 4

ADSI3393
ID ADSI3393 standard; peptide; 15 AA.

XX
AC ADSI3393;

```
XX 16-DEC-2004 (first entry)
DT
XX
DE Human rheumatoid arthritis marker peptide - SEQ ID 184.
XX
KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO2004082617-A2.
XX
PD 30-SEP-2004.
XX
PF 15-MAR-2004; 2004WO-US007880.
XX
PR 14-MAR-2003; 2003US-0455037P.
XX
PA (SURR-) SURROMED INC.
XX
PI Kantor AB, Becker CH, Schulman H;
XX
DR WPI; 2004-690929/67.
XX
PT New isolated marker for rheumatoid arthritis, useful in preparing a
PT composition for diagnosing or treating rheumatoid arthritis.
XX
PS Claim 1; SEQ ID NO 184; 184pp; English.
XX
SQ The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritic activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LMSGGGLNLCRPN 15
Db 1 LCMGSGGLNLCRPN 13
RESULT 5
ADSI3389
ID ADSI3389 standard; peptide; 15 AA.
XX
AC ADSI3389;
XX
XX 16-DEC-2004 (first entry)
DT
XX Human rheumatoid arthritis marker peptide - SEQ ID 180.
XX
DE Human rheumatoid arthritis marker; antiinflammatory; antiarthritic.
XX
KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO2004082617-A2.
XX
PD 30-SEP-2004.
XX
PF 15-MAR-2004; 2004WO-US007880.
```

```
XX 14-MAR-2003; 2003US-0455037P.
XX
XX (SURR-) SURROMED INC.
XX
PI Kantor AB, Becker CH, Schulman H;
XX
DR WPI; 2004-690929/67.
XX
PT New isolated marker for rheumatoid arthritis, useful in preparing a
PT composition for diagnosing or treating rheumatoid arthritis.
XX
PS Claim 1; SEQ ID NO 180; 184pp; English.
XX
SQ The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritic activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LMSGGGLNLCRPN 15
Db 1 LCMGSGGLNLCRPN 13
RESULT 6
ADV70473
ID ADV70473 standard; peptide; 15 AA.
XX
XX ADV70473;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human transferrin protein C-lobe region - SEQ ID 10.
XX
KW bacterial infection; antibacterial; bacterial meningitis; antibacterial;
KW neuroprotective; otitis media; auditory; transferrin.
XX
XX Homo sapiens.
XX
PN US2004258695-A1.
XX
PD 23-DEC-2004.
XX
PF 30-JAN-2004; 2004US-00769514.
XX
PR 31-JAN-2003; 2003US-0444113P.
XX
PA (SCHR/) SCHRIVERS A B.
XX
PI Schryvers AB;
XX
DR WPI; 2005-038740/04.
XX
PT Transferrin-binding molecules useful for eliciting antibodies to
PT bacterial transferrin binding proteins, which block bacterial transferrin
PT uptake.
XX
```

PS Claim 5; SEQ ID NO 10; 27pp; English.
XX
CC The invention comprises a molecule (e.g. peptide) which is capable of:
CC binding to a region of a transferrin protein that is recognized by a
CC bacterial transferrin binding protein; and eliciting an antibody to the
CC bacterial transferrin binding protein. The transferrin binding molecule
CC of the invention is useful for preventing and treating bacterial
CC infections (e.g. bacterial meningitis and otitis media). The present
CC amino acid sequence represents a region of the human transferrin protein
CC that is recognized by a bacterial transferrin binding protein.
XX
SQ Sequence 15 AA;

Query Match 74.3%; Score 55; DB 9; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LSMGSGNLSEPN 15
DB 1 LCMGSGNLCEPN 13

RESULT 7
ADV70505
ID ADV70505 standard; peptide; 15 AA.
XX
AC ADV70505;
XX
DT 10-MAR-2005 (first entry)
XX
DE Transferrin binding protein B-binding peptide - SEQ ID 42.
XX
KM bacterial infection; antibacterial; bacterial meningitis; antibacterial;
KM neuroprotective; otitis media; auditory; transferrin binding protein B.
XX
OS Unidentified.
XX
PN US2004258695-A1.
XX
PD 23-DEC-2004.
XX
PF 30-JAN-2004; 2004US-00769514.
XX
PR 31-JAN-2003; 2003US-0444113P.
XX
PA (SCHR/) SCHRYVERS A B.
XX
PI Schryvers AB;
XX
DR WPI; 2005-038740/04.
XX
PT Transferrin-binding molecules useful for eliciting antibodies to
PT bacterial transferrin binding proteins, which block bacterial transferrin
PT uptake.
XX
PS Example 2; SEQ ID NO 42; 27pp; English.
XX
CC The invention comprises a molecule (e.g. peptide) which is capable of:
CC binding to a region of a transferrin protein that is recognized by a
CC bacterial transferrin binding protein; and eliciting an antibody to the
CC bacterial transferrin binding protein. The transferrin binding molecule
CC of the invention is useful for preventing and treating bacterial
CC infections (e.g. bacterial meningitis and otitis media). The present
CC amino acid sequence represents a peptide that is bound by transferrin
CC binding protein B.
XX
SQ Sequence 15 AA;

Query Match 74.3%; Score 55; DB 9; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LSMGSGNLSEPN 15

DB 1 LCMGSGNLCEPN 13

RESULT 8
ADX17184
ID ADX17184 standard; peptide; 15 AA.
XX
AC ADX17184;
XX
DT 21-APR-2005 (first entry)
XX
DE Human serum albumin (HSA) peptide fragment, SEQ ID 82.
XX
KM protein purification; chromatography; screening.
XX
OS Homo sapiens.
XX
PN WO2005011576-A2.
XX
PD 10-FEB-2005.
XX
PF 23-JUL-2004; 2004WO-US023908.
XX
PR 25-JUL-2003; 2003US-0490149P.
XX
PA (BEYO-) BEYOND GENOMICS INC.
XX
PI Regnier FE, Ademec J, Zhang X;
XX
DR WPI; 2005-162781/17.
XX
PT Analyzing mixture of proteins by sequencing portions of peptides in two
PT or more sets of peptides from several peptides, to produce data set,
PT determining likelihood of presence of proteins in mixture of proteins
PT based on data sets.
XX
PS Example 4; SEQ ID NO 82; 140pp; English.
XX
CC The invention relates to a novel method for analyzing a mixture of
CC proteins. The method involves selecting sets of peptides from several
CC peptides, sequencing one or more portions of the peptides in two or more
CC sets of peptides, to produce a data set, and determining the likelihood
CC of the presence of two or more proteins in the mixture of proteins based
CC on two or more data sets. The invention further comprises an article of
CC manufacture comprising a computer-readable media with computer-readable
CC instructions for carrying out the method. The method is useful for
CC analyzing a mixture of proteins. The method is useful for screening and
CC characterization of protein mixtures. This sequence represents a human
CC serum albumin (HSA) peptide fragment used in the novel protein analysis
CC method of the invention.
XX
SQ Sequence 15 AA;

Query Match 74.3%; Score 55; DB 9; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LSMGSGNLSEPN 15
DB 1 LCMGSGNLCEPN 13

RESULT 9
ADV23202
ID ADV23202 standard; peptide; 15 AA.
XX
AC ADV23202;
XX
DT 10-MAR-2005 (first entry)
XX
DE HBV immunogenic peptide #3.
XX

KM Vaccine; virucide; antigen; autoimmune disease; infection;
KM Immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
KM breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
KM pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
KM Hodgkin's lymphoma.
XX
OS Hepatitis B virus.
XX
PN WO2004108753-A1.
XX
PD 16-DEC-2004.
XX
PF 10-JUN-2004; 2004WO-AU000775.
XX
XX 10-JUN-2003; 2003AU-00902875.
PR 25-MAR-2004; 2004AU-00901589.
XX
PA (UUME) UNIV MELBOURNE.
XX
PI Kent SJ;
XX
DR WPI; 2005-031657/03.
XX
PT Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
PS Disclosure; SEQ ID NO 1622; 645pp; English.
XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for modulating an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease
CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The unclonated
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC of aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
CC B virus protein.
XX
SQ Sequence 15 AA;
Query Match 47.3%; Score 35; DB 9; Length 15;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 3 | | | | |
GMSGTNSVNP 12
RESULT 10
ID AAY70486 standard; protein; 15 AA.
XX AAY70486;
XX
AC AAY70486;
XX
DT 04-JUL-2000 (first entry)
XX
XX Synthesised peptide-1 from human prothrombin kringle-2 protein.
XX
XX Human prothrombin kringle-2; prothrombin; kringle domain; cancer therapy;
KM anti-endothelial cell proliferation; anti-tumour; angiogenesis; cancer;
KM skin; laryngeal; uterine; colon; lung; bone marrow; cytostatic;
KM anti-angiogenic.
XX
XX Homo sapiens.
OS
XX
XX WO200014209-A1.
XX
XX 16-MAR-2000.
PD
XX
XX 07-SEP-1999; 99WO-KR000525.
PF
XX
XX 07-SEP-1998; 98KR-00036786.
PR
XX
XX (KIMS/) KIM S.S.
PA (GENO-) GENOTECH CORP.
XX
XX Rhim TY, Park CS, Kim EK;
PI
XX
XX WPI; 2000-256965/22.
DR
XX
XX Human prothrombin kringle-1 and kringle-2 polypeptides that inhibit
PT angiogenesis, useful for treating cancer.
PT
XX
XX Example 7; Page 19; 43pp; English.
XX
XX The present sequence is a synthesised peptide of human prothrombin
CC kringle-2 protein which is derived from human plasma prothrombin.
CC Peptides were synthesised having amino acid sequences in order from N-
CC terminal sequence of prothrombin kringle-2 by overlapping 2-5 amino acids
CC of both N-terminal and C-terminal of peptides. These peptides were
CC purified by high performance liquid chromatography (HPLC). Kringle
CC domains from prothrombin have anti-endothelial cell proliferation and
CC anti-tumour activities. These inhibit angiogenesis which is involved in
CC tumour growth. They are also useful for the treatment of cancer, e.g.
CC skin, laryngeal, uterine, colon, lung and bone marrow cancer. The human
CC prothrombin kringle-2 significantly suppresses tumour growth in vivo
XX
SQ Sequence 15 AA;
Query Match 44.6%; Score 33; DB 3; Length 15;
Best Local Similarity 63.6%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 4 SMSGTNSVNP 14
DB 1 | | | | |
SEGSSVNLSP 11
RESULT 11
ADV23201
ID ADV23201 standard; peptide; 15 AA.
XX
XX ADV23201;
AC
XX
DT 10-MAR-2005 (first entry)
XX
XX HBV immunogenic peptide #2.
DE

XX Vaccine; virucide; antigen; autoimmune disease; infection;
 KM immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KM breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KM pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KM hodgkin's lymphoma.
 XX
 OS Hepatitis B virus.
 XX
 PN WO2004108753-A1.
 XX
 PD 16-DEC-2004.
 XX
 PF 10-JUN-2004; 2004WO-AU000775.
 XX
 PR 10-JUN-2003; 2003AU-00902875.
 XX 25-MAR-2004; 2004AU-00901589.
 XX
 PA (UYME) UNIV MELBOURNE.
 XX
 PI Kent SJ;
 XX
 DR WPI; 2005-031657/03.
 XX
 PT Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.
 XX
 PS Disclosure; SEQ ID NO 1621; 645pp; English.
 XX
 XX The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other
 CC peptide of the same set of peptides (i.e. they are overlapping). Also
 CC included are an antigen-presenting cell which has been contacted with the
 CC peptides above and thus presents the peptides, a population of such
 CC antigen-presenting cells, a process for producing antigen-presenting
 CC cells for modulating an immune response to a polypeptide of interest, a
 CC method for producing antigen-specific lymphocytes, a composition
 CC comprising at least one set of the peptides (and a carrier and/or
 CC diluent), a method for modulating an immune response to a polypeptide of
 CC interest comprising administering to a patient in need at least one set
 CC of the peptides, a method for treatment and/or prophylaxis of a disease
 CC or condition associated with the presence of a polypeptide of interest
 CC and a composition of matter for modulating an immune response in a
 CC subject to a target antigen. The polypeptide of interest is also a
 CC disease- or condition-associated polypeptide that is a polypeptide
 CC produced by a pathogenic organism or a cancer, and produced by a
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
 CC protozoans and mycoplasmas. The disease- or condition-associated
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
 CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
 CC antigen-presenting cells or their precursors are useful in the
 CC preparation of a medicament for the treatment of a disease or condition
 CC in a subject, which disease or condition is associated with the presence
 CC or aberrant expression of a target antigen, where the antigen-presenting
 CC cells or their precursors have not been subjected to activating
 CC conditions but have been contacted with an antigen that corresponds to
 CC the target antigen to express a processed or modified form of the antigen
 CC for presentation to the subject's immune system. The present sequence is
 CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
 CC B virus protein.
 XX
 SO Sequence 15 AA;

Query Match 44.6%; Score 33; DB 9; Length 15;
 Best Local Similarity 57.1%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SKLSWGSGLNLSP 14
 || | | | | | |
 Db 2 SKPRKMGKTNLSVP 15
 || | | | | | |
 RESULT 12
 AAR62914
 ID AAR62914 standard; protein; 15 AA.
 XX
 AC AAR62914;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-JUN-1995 (first entry)
 XX
 DE V-alpha chain CDR3 J-alpha region.
 XX
 KM Allergen; immunotherapy; T-cell receptor; TCR; CDR;
 KM complementarity determining region; immunosuppressive;
 KM antibody engineering; suppressor T-lymphocyte; T_H; ovalbumin;
 KM monoclonal antibody; myeloma; IgG.
 XX
 OS Synthetic.
 XX
 PN WO9425489-A1.
 XX
 PD 10-NOV-1994.
 XX
 PF 26-APR-1994; 94WO-CA000228.
 XX
 PR 26-APR-1993; 93GB-0008581.
 XX
 PA (UYMA-) UNIV MANITOBA.
 XX
 PI Mohapatra SS, Sehon AH;
 XX
 DR WPI; 1994-358193/44.
 XX
 PT Synthetic peptide(s) for effecting immunotherapy - have an amino acid
 PT sequence comprising a portion of the CDR3 region of a T-cell receptor.
 XX
 PS Disclosure; Page 44; 78pp; English.
 XX
 XX Antibody production against allergenic antigen (Ag) is specifically
 CC suppressed by treatment with the junctional segment of the alpha and/or
 CC beta chain of the Ag receptor of suppressor T (T_S) cells (T_{CR}) induced by
 CC tolerogenic Ag-P₈₆ conjugates. Induction of antigen-specific suppression
 CC by treatment of mice with TCR alpha-chain peptides was demonstrated using
 CC the peptides given in AAR62912-17. The peptide of AAR62914 corresponds to
 CC the J-alpha region of the CDR3 segment of the alpha chain of ovalbumin-
 CC specific T_S cells. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SO Sequence 15 AA;

Query Match 40.5%; Score 30; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SKLSWGSGLNLSP 12
 : | | | | | |
 Db 4 AKLTFGKGTWLS 15
 : | | | | | |
 RESULT 13
 AAR94866
 ID AAR94866 standard; peptide; 15 AA.
 XX
 AC AAR94866;
 XX
 DT 11-NOV-1996 (first entry)
 XX
 DE Peptide from library spanning whole of hsp65.
 XX
 KM Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;

CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention
 XX

SQ Sequence 15 AA;

Query Match 40.5%; Score 30; DB 5; Length 15;
 Best Local Similarity 75.0%; Pred. NO. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GLNLSEPN 15
 | | | | |
 Db 1 GTNLSTVPN 8

Search completed: June 13, 2006, 02:42:03
 Job time : 197 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:42:20 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-612-162A-3
Perfect score: 74
Sequence: 1 SKLMSGSLNLSPPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 427

Minimum DB seq length: 15
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	28.4	15	2	S21238	Hydrogensulfite re
2	21	28.4	15	2	C36198	T-cell receptor be
3	21	28.4	15	2	A36315	recycling receptor
4	21	28.4	15	2	PH1455	T-cell receptor al
5	20	27.0	15	2	S49409	H+-transporting tw
6	20	27.0	15	2	A56049	urinary tract ston
7	19	25.7	15	2	S26527	T-cell receptor al
8	19	25.7	15	2	S43634	cytochrome-c oxida
9	18	24.3	15	2	PH0775	T-cell receptor al
10	18	24.3	15	2	PH0784	T-cell receptor al
11	18	24.3	15	2	PH0751	T-cell receptor be
12	18	24.3	15	2	S05699	insulin-like growt
13	18	24.3	15	2	G24417	interphotoreceptor
14	17	23.0	15	2	PC2215	fibrinogenolytic p
15	17	23.0	15	2	F29501	fibronectin A -
16	17	23.0	15	2	B56661	S-locus specific g
17	17	23.0	15	2	G41299	T-cell receptor al
18	17	23.0	15	2	PH0074	T-cell receptor be
19	17	23.0	15	2	PH0080	T-cell receptor al
20	17	23.0	15	2	PA0006	lectin A3 - Psopho
21	17	23.0	15	2	PA0075	fructose-bisphosph
22	16.5	22.3	15	2	A22789	platelet-derived g
23	16	21.6	15	2	B61243	dimethylamine mo
24	16	21.6	15	2	S57201	basic proteinase 1
25	16	21.6	15	2	A38304	heterogeneous ribo
26	16	21.6	15	2	PA0055	protein QP200007 -
27	16	21.6	15	2	PH0136	T-cell receptor be
28	16	21.6	15	2	C24687	T-cell receptor be
29	16	21.6	15	2	S66215	cartilage oligomer

30	16	21.6	15	2	E56978	collagen alpha 2 (X
31	16	21.6	15	2	A42413	Ig heavy chain V r
32	16	21.6	15	2	PH0779	T-cell receptor al
33	16	21.6	15	2	PH0782	T-cell receptor al
34	16	21.6	15	2	PA0102	fructose-bisphosph
35	16	21.6	15	2	PA0079	malate dehydrogena
36	16	21.6	15	2	C32521	hexokinase (EC 2.7
37	16	21.6	15	2	S62509	glutathione-disulf
38	16	21.6	15	2	S60341	protein kinase (EC
39	15	20.3	15	2	S26524	T-cell receptor al
40	15	20.3	15	2	D48394	major fat-globule
41	15	20.3	15	2	S65717	prostaglandin D-sy
42	15	20.3	15	2	PA0039	protein OA100039 -
43	15	20.3	15	2	PS0208	20K protein 5403 -
44	15	20.3	15	2	C61511	milk band B protei
45	15	20.3	15	2	PH1314	Ig heavy chain DJ

ALIGNMENTS

RESULT 1

S21238
hydrogensulfite reductase (EC 1.8.99.3) beta chain - Desulfovibrio vulgaris (fragment)
N;Alternate names: disulfite reductase; desulfotetradin; desulfotetradin; desulfotetradin;
C;Species: Desulfovibrio vulgaris
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S21238
R;Pierik, A.J.; Duyvis, M.G.; van Heijvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.
Eur. J. Biochem. 205, 11-15, 1992
A;Title: The third subunit of desulfovibrio-type dissimilatory sulfite reductases.
A;Reference number: S21197; PMID:92209491; PMID:1555572
A;Accession: S21238
A;Molecule type: protein
A;Residues: 1-15 <PIE>
A;Cross-references: UNIPARC:UP1000017AB71
A;Experimental source: strain Hildenborough
C;Genetics:
A;Gene: dsyb
A;Complex: heterodimer; two alpha, two beta and two gamma chains
C;Function:
A;Description: catalyzes the six-electron reduction of sulfite to sulfide
A;Pathway: the terminal oxidase in the sulfate-reduction pathway
C;Keywords: heterodimer; oxidoreductase

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 MSGSLNLSPPN 14
Db : ||| :
3 ISSGYNPEKP 12

RESULT 2

C36198
T-cell receptor beta chain J region - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 21-Jul-2000
C;Accession: C36198
R;Tjoelker, L.W.; Carlson, L.M.; Lee, K.; Lahti, J.; McCormack, W.T.; Leiden, J.M.; Chen
Proc. Natl. Acad. Sci. U.S.A. 87, 7856-7860, 1990
A;Title: Evolutionary conservation of antigen recognition: the chicken T-cell receptor be
A;Reference number: A36198; PMID:91045896; PMID:2236002
A;Accession: C36198
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-15 <TIO>
A;Cross-references: UNIPARC:UP100001151E; EMBL:M37799; NID:G212737; PIDD:AAA62754.1; PIDD:
C;Keywords: T-cell receptor

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;

```
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 LSWGSGLNLS 12
| : | | |
Db 4 LNFQGTRLT 13

RESULT 3
A36315
recycling receptor p180 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 30-Sep-1993
C:Accession: A36315
R:Jacks, C.M.; Van der Geer, P.; Hunter, T.; Trowbridge, I.S.
Mol. Cell. Biol. 10, 2606-2618, 1990
A>Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type ex
A:Reference number: A36315; PMID:90258846; PMID:2188094
A:Accession: A36315
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <ISA>
A:Cross-references: UNIPARC:UPI000017C337

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 LSEPN 15
| | |
Db 7 LPEPN 11

RESULT 4
PH1455
T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1455
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A>Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; PMID:93171821; PMID:8436911
A:Accession: PH1455
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI000017C762
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSWGSGL 9
| | |
Db 3 LNRGSL 9

RESULT 5
S49409
H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Streptococcus oralis (fragment)
C:Species: Streptococcus oralis
C>Date: 29-Nov-1995 #sequence_revision 01-Aug-1997 #text_change 31-Dec-2004
C:Accession: S49409; S38211
R:Fennil, A.; Munoz, R.; Garcia, E.; de la Campa, A.G.
Mol. Microbiol. 12, 587-598, 1994
A>Title: Molecular basis of the optochin-sensitive phenotype of pneumococcus: characteri
ases
A:Reference number: S49398; PMID:95020593; PMID:7934882
A:Accession: S49409
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <FEN>
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```
A:Cross-references: UNIPROT:Q60249; UNIPARC:UPI0000170206; EMBL:Z26853; NID:G407180; PID
C:Superfamily: H(+)-transporting ATP synthase protein 6
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 30.8%; Pred. No. 2.7e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SKLSGSGLNLS 13
| : | | |
Db 2 SSMYLNKINDGE 14

RESULT 6
A56049
urinary tract stone matrix protein, 40K - unidentified organism (fragment)
C:Species: unidentified organism
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 20-Apr-2000
C:Accession: A56049
R:Binette, J.P.; Binette, M.B.
Scanning Microsc. 8, 233-239, 1994
A>Title: Sequencing of proteins extracted from stones.
A:Reference number: A56049; PMID:95215817; PMID:7701298
A:Accession: A56049
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BIN>
A:Cross-references: UNIPARC:UPI0000071BE1
A:Experimental source: urinary tract and gallbladder stones
A>Note: the source is designated as Homo sapiens, however the true source probably origi

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 MGSGLNLS 13
| | |
Db 3 VGGGATLPE 11

RESULT 7
S26527
T-cell receptor alpha chain V region (clone Cw3/A8, A3/74.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
A:Variety: clone Cw3/A8; A3/74.1
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26527; PH1442
R:Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Widh
J. Exp. Med. 176, 439-447, 1992
A>Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; PMID:92364546; PMID:1380061
A:Accession: S26527
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI00001769BB; EMBL:X67978
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A>Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; PMID:93171821; PMID:8436911
A:Accession: PH1442
A:Molecule type: mRNA
A:Residues: 1-15 <CAN>
A:Cross-references: UNIPARC:UPI00001769BB
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LSWG 6
```

Db 3 LSMG 6

RESULT 8

S43634
Cytochrome-c oxidase (EC 1.9.3.1) chain V1C, cardiac - rainbow trout (fragment)
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C/Accession: S43634
R/Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A/Title: Identification of tissue-specific isoforms for subunits Vb and V1a of cytochrome c oxidase
A/Reference number: S43624; MUID:94237150; PMID:8181465
A/Accession: S43634
A/Molecule type: protein
A/Residues: 1-15 <FRE>
A/Cross-references: UNIPARC:UPI000017BF5A
A/Note: the source is designated as Salmo gairdneri
C/Genetics:
A/Genome: nuclear
C/Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSGGNTL 11
| | | |
Db 6 GPGGNTL 11

RESULT 9

PH0775
T-cell receptor alpha chain (B28) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0775
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0775
A/Molecule type: mRNA
A/Residues: 1-15 <CAS>
A/Cross-references: UNIPARC:UPI000017C75A; EMBL:X60871
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 4.1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSL 9
| | | |
Db 3 LSGGSL 9

RESULT 10

PH0784
T-cell receptor alpha chain (F1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0784
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0784
A/Molecule type: mRNA
A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI000017C75B; EMBL:X60885
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 24.3%; Score 18; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 LSEPN 15
| | | |
Db 3 LSDPS 7

RESULT 11

PH0751
T-cell receptor beta chain (F12) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0751
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0751
A/Molecule type: mRNA
A/Residues: 1-15 <CAS>
A/Cross-references: UNIPARC:UPI000015F5AA; EMBL:X60843; MUID:950931; PIDN:CAA43235.1; PIDN:CAA43235.1; PIDN:CAA43235.1
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 24.3%; Score 18; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SMGSG 8
| | | |
Db 3 SIGTG 7

RESULT 12

S05699
Insulin-like growth factor-binding protein, juvenile - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S05699
R/Rochant, M.; Hoesenlopp, P.; Lepage, P.; Balland, A.; Binoux, M.
FEBS Lett. 255, 253-258, 1989
A/Title: Isolation from human cerebrospinal fluid of a new insulin-like growth factor-binding protein
A/Reference number: S05699; MUID:90005986; PMID:2551732
A/Accession: S05699
A/Molecule type: protein
A/Residues: 1-15 <ROG>
A/Cross-references: UNIPROT:P24592; UNIPARC:UPI000017C276

Query Match 24.3%; Score 18; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 GSGGNTL 14
| | | |
Db 6 GGGVQAGAP 14

RESULT 13

G24417
Interphotoreceptor retinoid-binding protein - hamster (fragment)
N/Alternate names: Interstitial retinol-binding protein
C/Species: Cricetinae gen. sp. (hamster)
C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C/Accession: G24417
R/Pong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986

A>Title: N-terminal sequence homologues in interstitial retinol-binding proteins from 10
A:Reference number: A91365; MUID:86301171; PMID:3743780
A:Accession: G24417
A:Molecule type: protein
A:Residues: 1-15 <FON>
A:Cross-references: UNIPROT:P12665; UNIPARC:UPI000012D879

Query Match 24.3%; Score 18; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 NLSEPN 15
| | |
| | |
Db 5 NLFQPS 10

RESULT 14

PC2215
fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragment
N/Alternate names: alpha-fibrinogenase A2
C/Species: Crotales atrox (western diamondback rattlesnake)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: PC2215
R/Hung, C.C.; Chiu, S.H.
Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994
A>Title: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamond
viper.
A:Reference number: PC2214; MUID:94296418; PMID:8024586
A:Accession: PC2215
A:Molecule type: protein
A:Residues: 1-15 <HUN>
A:Cross-references: UNIPROT:Q9PRW3; UNIPARC:UPI00000FD6F1
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase

Query Match 23.0%; Score 17; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 9.6e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGNLSE 13
| | |
| | |
Db 4 GDECNINE 11

RESULT 15

F29501
fibrinopeptide A - wombat
C/Species: Vombatidae gen. sp. (wombat)
C/Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
C/Accession: F29501
R/Blomback, B.; Blomback, M.; Hann, C.
Unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: F29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BKO>
A:Cross-references: UNIPROT:Q7M318; UNIPARC:UPI00001777D7
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 23.0%; Score 17; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 9.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SKLSMSGSL 9
| | |
| | |
Db 6 SFLAEGGV 14

Search completed: June 13, 2006, 02:47:43
Job time : 39 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:38:55 ; Search time 291 Seconds

(without alignments)
47.681 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKLSMGSGNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 1126

Minimum DB seq length: 15
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	28.4	15	1	CMP01_LYCSES
2	21	28.4	15	2	065177_MESCR
3	21	28.4	15	2	03ZUF3_GRICK
4	20	27.0	15	1	FIBA_SYNCA
5	20	27.0	15	2	07S362_NEUCR
6	20	27.0	15	2	09TMB6_TRIGR
7	20	27.0	15	2	0798U8_STROR
8	20	27.0	15	2	084332_SV40
9	19.5	26.4	15	1	GSTR2_PSEUO
10	19.5	26.4	15	2	013377_HUMAN
11	19	25.7	15	2	086WB2_HUMAN
12	19	25.7	15	2	09WTA3_GABAE
13	19	25.7	15	2	03ZUD3_RICAK
14	19	25.7	15	2	03ZUD5_9RICK
15	19	25.7	15	2	03ZUD6_RICMA
16	19	25.7	15	2	03ZUD7_9RICK
17	19	25.7	15	2	03ZUD8_RICHE
18	19	25.7	15	2	03ZUD9_RICSI
19	19	25.7	15	2	03ZUD0_RICRI
20	19	25.7	15	2	03ZUD1_RICAR
21	19	25.7	15	2	03ZUD2_RICUA
22	19	25.7	15	2	03ZUD3_RICPA
23	19	25.7	15	2	03ZUD4_RICSA
24	19	25.7	15	2	03ZUD5_RICSI
25	19	25.7	15	2	03ZUD6_RICRI
26	19	25.7	15	2	03ZUD7_RICAK
27	19	25.7	15	2	03ZUD8_RICRI
28	19	25.7	15	2	03ZUD9_RICMA
29	19	25.7	15	2	03ZUD0_RICSI
30	19	25.7	15	2	03ZUD1_RICAR
31	18.5	25.0	15	2	09QV76_9MURI

32	18	24.3	15	1	IRBP_CRISP	P12665 cricetidae
33	18	24.3	15	2	R13A_SPROL	P82454 spinnacia ol
34	18	24.3	15	2	09UCY1_HUMAN	Q9UCY1 homo sapien
35	18	24.3	15	2	08N0N6_BRAFL	Q8N0N6 branchiost
36	18	24.3	15	2	09R4M7_BACFI	Q9R4M7 bacillus fi
37	18	24.3	15	2	09X635_ECOLI	Q9X635 escherichia
38	18	24.3	15	2	09X637_KLEEX	Q9X637 klebsiella
39	17	23.0	15	1	CMP18_PRAVU	P80777 phaseolus v
40	17	23.0	15	1	DNAC_COMAC	P83709 comamonas a
41	17	23.0	15	1	HLOB_HALAU	P83706 halocynthia
42	17	23.0	15	1	LECA3_PSOOC	P22583 psophocarpu
43	17	23.0	15	1	OBPA_MAMBR	P81285 mamestra br
44	17	23.0	15	1	UC25_MAIZE	P80631 zea mays (m
45	17	23.0	15	1	VSP3_AGKHP	P80899 agkistrodon

ALIGNMENTS

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RESULT 1
CMP01_LYCSES STANDARD; PRT; 15 AA.
ID CMP01_LYCSES
AC P80798;
DT 27-SEP-2005, integrated into UniProtKB/Swiss-Prot.
DT 27-SEP-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE 65 kDa cell wall protein (fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;
RA Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,
RA Slabas A.R.;
RT "Differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants.";
RL J. Biol. Chem. 272:15841-15848(1997).
CC -1- SUBCELLULAR LOCATION: Secreted; cell wall.
CC
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CC
KW Cell wall; Direct protein sequencing.
FT CHAIN 1
FT FT 65 kDa cell wall protein.
FT FT /Ftrid=PRO_0000079621.
FT NON TER 15
FT SEQUENCE 15 AA; 1574 MW; DA9E7BDBD9E7AD2C CRC64;
SQ
Query Match 28.4%; Score 21; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.7e+04;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 6 GSGINLSEP 14
Db 2 GKALGLAKP 10
RESULT 2
ID 065177_MESCR PRELIMINARY; PRT; 15 AA.
AC 065177;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Tumor responsive protein homolog (fragment).
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Alstroceae; Mesembryanthemum.
OX NCBI_TaxID=3544;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=ROCK.
RA Michalowski C.B., Bohmert H.J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL, AF054444; AAC14178.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 15 AA; 1607 MW; 4137ED0DF9B3FC21 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SKLMSGSLN 10
DB 4 NELPLAOGIN 13

RESULT 3
ID Q3JF3_9RICK PRELIMINARY; PRT; 15 AA.
AC Q3JF3_9RICK
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DE DksA (Fragment).
GN Name=dksA;
OS Rickettsia honei.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=37816;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TTT;
RA PubMed=16091434; DOI=10.1099/jmm.0.45956-0;
RA Vitorino L., de Sousa R., Baccellar F., Ze-Ze L.;
RT "Characterization of a tandem repeat polymorphism in Rickettsia
RT strains."
RL J. Med. Microbiol. 54:833-841 (2005).
CC -----
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CC -----
DR EMBL, AY820025; AAY40564.1; -, Genomic_DNA.
FT NON TER 15
SQ SEQUENCE 15 AA; 1724 MW; 9CE14537A1755B8 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLSMG 6
DB 6 KLTMG 10

RESULT 4
ID FIBA_SYNCA STANDARD; PRT; 15 AA.
AC P14453;
DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1990, sequence version 1.
DE 07-FEB-2006, entry version 29.
DE Fibrinogen alpha chain [contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Syncerus caffer (Cape buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Syncerus.

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OX NCBI_TaxID=9970;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;
RT "Amino acid sequence studies on arctodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo."
RL Arch. Biochem. Biophys. 118:456-467 (1967).
CC -----
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterochimers
CC are in head to head conformation with the N-termini in a small
CC central domain (by similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central node to the C-terminal domains
CC (distal nodes). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC -----
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CC -----
DR EMBL, AF054444; AAC14178.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;

Query Match 27.0%; Score 20; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.6e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSGGLNSE 13
DB 3 GSGGLNSE 10

RESULT 5
ID Q7S362_NEUCR PRELIMINARY; PRT; 15 AA.
AC Q7S362;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 8.
DE Predicted protein.
GN ORFNames=NCU08588.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 9871.
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smolnov S., Purcell S., Rehan B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A., Braun E.L.,
RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jed G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Strange-Thomann N., Barrett R., Gnere S., Kamal M., Kamysseis M.,
RA Muccelli E., Bielke C., Rudd S., Friseman D., Kravtsova S.,
RA Kasumussen C., Metzgerberg R.L., Perkins D.D., Oksanen S., Cogoni C.,
RA Macino G., Catchside D.E.A., Li W., Pratt R.J., Oshani S.A.,
RA Desouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Veilker R.,
RA Yarden O., Plamann M., Selzer S., Dunlap J.C., Radford A., Aramayo R.,

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RA  Nativig D.O., Alex L.A., Mannheim G., Ebojie D.J., Freitag M.,
RA  Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.W.;
RT  "The genome sequence of the filamentous fungus Neurospora crassa.";
RL  Nature 422:859-868(2003).
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
CC  -----
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CC
DR  EMBL: AABX0100413; EAA29870.1; -; Genomic DNA.
SQ  SEQUENCE 15 AA; 1753 MW; 44BAA4C5D52DA9A CRC64;

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 38.5%; Pred. No. 2.6e+04;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SKLMSGSLINSE 13
DB 2 SDSLINIKINDGE 14

RESULT 6
Q9TWB6_TRIGR PRELIMINARY; PRT; 15 AA.
AC Q9TWB6;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Protease (Fragment).
OS Tripneustes gratilla (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Tripneustes.
OC NCBI_TaxID=7673;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020861; PubMed=1717978;
RA Springer M.S., Davidson E.H., Britten R.J.;
RT "Retroviral-like element in a marine invertebrate.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8401-8404(1991).
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CC
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1616 MW; 2C372951BC4DBE56 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.6e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSMSGSLINL 11
DB 4 KIDTGAQANL 13

RESULT 7
Q798U8_STROR PRELIMINARY; PRT; 15 AA.
AC Q798U8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Adenosine triphosphatase (EC 3.6.1.3) (Fragment).
GN Name=atpA;
OS Streptococcus oralis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1303;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11427;
RX MEDLINE=95020593; PubMed=7934882;
RA Ferrell A., Munoz R., Garcia E., de la Campa A.G.;
RT "Molecular basis of the optochin-sensitive phenotype of pneumococcus:
RT characterization of the genes encoding the F0 complex of the
RT Streptococcus pneumoniae and Streptococcus oralis H(+)-ATPases.";
RL Mol. Microbiol. 12:587-598(1994).
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CC
DR EMBL: Z26853; CAAB1457.1; -; Genomic DNA.
DR GO: GO:0042624; F:ATPase activity, uncoupled; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1670 MW; 0ADE2A58DBD9D248 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 30.8%; Pred. No. 2.6e+04;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SKLMSGSLINSE 13
DB 2 SSWTLGNKINDGE 14

RESULT 8
Q84332_SV40 PRELIMINARY; PRT; 15 AA.
ID Q84332_SV40
AC Q84332;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Minor structural protein VP2 (Fragment).
OS Simian virus 40 (SV40).
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OC NCBI_TaxID=10633;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EK;
RX MEDLINE=78156432; PubMed=205802;
RA Fiers W., Concleris R., Haegeman G., Rogiers R., van de Voorde A.,
RA van Heuverswyn H., van Herreweghe J., Volckaert G., Ysebaert M.;
RT "Complete nucleotide sequence of SV40 DNA.";
RL Nature 273:113-120(1978).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EK;
RX MEDLINE=78159686; PubMed=205947;
RA Reddy V.B., Thimmappaya B., Dhar R., Subramanian K.N., Zain B.S.,
RA Pan J., Ghosh P.K., Celma M.L., Weissman S.M.;
RT "The genome of simian virus 40.";
RL Science 200:494-502(1978).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EK;
RX MEDLINE=80024255; PubMed=226361;
RA van Heuverswyn H., Fiers W.;
RT "Nucleotide sequence of the Hind-C fragment of Simian virus 40 DNA:
RT comparison of the 5'-untranslated region of wild-type virus and of
RT some deletion mutants.";
RL Eur. J. Biochem. 100:51-60(1979).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EK;
RX MEDLINE=93021360; PubMed=1328671;
RA Ilyinskii P.O., Daniel M.D., Horvath C., Desrosiers R.C.;
RT "Genetic analysis of simian virus 40 from brains and kidneys of
RT macaque monkeys.";
RL J. Virol. 66:6353-6360(1992).
CC -----

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 CC -----
 DR EMBL: M99363; AAB59779.1; -; Genomic_DNA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR001070; Polyoma coat2.
 DR Pfam: PF00761; Polyoma coat2; 1.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1459 MW; 40EDDFPC02786C4E CRC64;
 QY Query Match 27.0%; Score 20; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.6e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 5 MSGSLN 11
 1 MGALTL 7
 RESULT 9
 GSTE2_PSEUDO STANDARD; PRT; 15 AA.
 AC P83000;
 DT 10-MAY-2004; Integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2002; sequence version 1.
 DE 07-FEB-2006; entry version 16.
 DE Glutathione S-transferase (EC 2.5.1.18) (Fragment).
 OS Pseudomonas sp. (strain M1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=95619;
 RN [1]
 RP PROTEIN SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND
 RP SUBCELLULAR LOCATION.
 RA MEDLINE=21896940; PubMed=11900268; DOI=10.1016/S0923-2508(01)01293-1;
 RA Santos P.M., Mignogna G., Heideper H.J., Zennaro E.;
 RT "Occurrence and properties of glutathione S-transferases in phenol-
 RT degrading Pseudomonas strains";
 RL Res. Microbiol. 153:89-98(2002).
 CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of
 CC exogenous and endogenous hydrophobic electrophiles.
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -1- SUBUNIT: Monomer and homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasm.
 CC -1- SIMILARITY: Belongs to the GST superfamily.
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 CC -----
 DR GO: GO:0005737; C:cytoplasm; NAS.
 DR GO: GO:0004364; F:glutathione transferase activity; NAS.
 KW Direct protein sequencing; Transferase.
 FT CHAIN 1 >15
 /FTID=PRO_0000185980.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1608 MW; 571C90DA7595077A CRC64;
 QY Query Match 26.4%; Score 19.5; DB 1; Length 15;
 Best Local Similarity 53.8%; Pred. No. 3.2e+04;
 Matches 7; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Db 3 LSMGSLN 15
 3 LVIGS-KNLSSTN 14
 RESULT 10
 Q13377_HUMAN PRELIMINARY; PRT; 15 AA.
 AC Q13377;
 DT 01-NOV-1996; Integrated into UniProtKB/TrEMBL.
 DT 01-FEB-2005; sequence version 3.

DT 07-FEB-2006; entry version 18.
 DE RNA binding motif (Fragment).
 GN Name=RBW;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97032533; PubMed=8875892; DOI=10.1007/s003359900246;
 RA Prosser J., Inglis J.D., Condie A., Ma K., Kerr S., Thakrar R.,
 RA Taylor K., Cameron J.M., Cooke H.J.;
 RT "Degeneracy in human multicopy RBM (YRRM), a candidate spermatogenesis
 RT gene";
 RL Mamm. Genome 7:835-842(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Taylor K.E., Cameron J.M.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: U38451; ABA49816.1; -; Genomic_DNA.
 DT 07-FEB-2006; entry version 8.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1713 MW; 12D127D52A2820A3 CRC64;
 QY Query Match 26.4%; Score 19.5; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.2e+04;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 Db 2 KLSMSGSLN 10
 1 KLFIF-GLN 8
 RESULT 11
 Q86WB2_HUMAN PRELIMINARY; PRT; 15 AA.
 ID Q86WB2;
 AC Q86WB2;
 DT 01-JUN-2003; Integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003; sequence version 1.
 DE 07-FEB-2006; entry version 8.
 DE Acetyl-CoA carboxylase-alpha (EC 6.4.1.2) (Fragment).
 GN Name=ACACA;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RA Travers M.T., Barber M.C.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: A053489; CAD59557.1; -; mRNA.
 DR GO: GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 KW Ligase.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1753 MW; 56E3033C9FDS56EA CRC64;
 QY Query Match 25.7%; Score 19; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.9e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 7 SGLNLT 11

Db 2 SGLHL 6

RESULT 12

Q9WTA3_9ARAE PRELIMINARY; PRT; 15 AA.

AC Q9WTA3;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE ACPB protein (Fragment).
GN Name=acpB;
OS Amorphnallus hirtus.
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Aroidaceae;
OC Thomontaceae; Amorphnallus.
OX NCBI_TaxId=74664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chiang T.Y., Peng C.I.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

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EMBL: AJ224958; CAB39368.1; -; Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1547 MW; 8875F4EB641DED5C CRC64;

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.9e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 SGLNLS 12
Db 8 SGLGVS 13

RESULT 13

Q3ZUD3_RICAK PRELIMINARY; PRT; 15 AA.

AC Q3ZUD3;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE DksA (Fragment).
GN Name=dksA;
OS Rickettsia akari.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxId=786;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RX PubMed=16091434; DOI=10.1099/jmm.0.45956-0;
RA Vitorino L., de Sousa R., Bacellar F., Ze-Ze L.;
RT "Characterization of a tandem repeat polymorphism in Rickettsia strains";
RT J. Med. Microbiol. 54:833-841(2005).
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EMBL: AY820045; AAY40584.1; -; Genomic_DNA.
DR NON_TER 15
SQ SEQUENCE 15 AA; 1720 MW; 28E145337A1304BE CRC64;

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.9e+04;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLSWG 6
Db 6 KLPWG 10

RESULT 14

Q3ZUD4_RICRH PRELIMINARY; PRT; 15 AA.

AC Q3ZUD4;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE DksA (Fragment).
GN Name=dksA;
OS Rickettsia rhipicephali.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxId=33992;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RX PubMed=16091434; DOI=10.1099/jmm.0.45956-0;
RA Vitorino L., de Sousa R., Bacellar F., Ze-Ze L.;
RT "Characterization of a tandem repeat polymorphism in Rickettsia strains";
RT J. Med. Microbiol. 54:833-841(2005).
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EMBL: AY820044; AAY40583.1; -; Genomic_DNA.
DR NON_TER 15
SQ SEQUENCE 15 AA; 1720 MW; 28E145337A1755BE CRC64;

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.9e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLSWG 6
Db 6 KLPWG 10

RESULT 15

Q3ZUD5_9RICK PRELIMINARY; PRT; 15 AA.

AC Q3ZUD5;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE DksA (Fragment).
GN Name=dksA;
OS Rickettsia aeschlimanni.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxId=45262;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RX PubMed=16091434; DOI=10.1099/jmm.0.45956-0;
RA Vitorino L., de Sousa R., Bacellar F., Ze-Ze L.;
RT "Characterization of a tandem repeat polymorphism in Rickettsia strains";
RT J. Med. Microbiol. 54:833-841(2005).
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EMBL: AY820043; AAY40582.1; -; Genomic_DNA.
DR NON_TER 15
SQ SEQUENCE 15 AA; 1720 MW; 28E145337A1755BE CRC64;

Query Match 25.7%; Score 19; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.9e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KLSMG 6
Db 6 KLPWG 10

Search completed: June 13, 2006, 02:46:59
Job time : 293 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:47:16 ; Search time 49 Seconds
(without alignments)
26.795 Million cell updates/sec

Title: US-10-612-162a-3
Sequence: 1 SKLMSGSLNLEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 17069

Minimum DB seq length: 15
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /EMC_Ceiera_SIDS3/prodata/2/iaa/6.COMB.pep.*
3: /EMC_Ceiera_SIDS3/prodata/2/iaa/7.COMB.pep.*
4: /EMC_Ceiera_SIDS3/prodata/2/iaa/H.COMB.pep.*
5: /EMC_Ceiera_SIDS3/prodata/2/iaa/PCMS.COMB.pep.*
6: /EMC_Ceiera_SIDS3/prodata/2/iaa/RE.COMB.pep.*
7: /EMC_Ceiera_SIDS3/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	40.5	15	2	US-09-239-043D-2101
2	27	36.5	15	2	US-09-239-043D-2101
3	27	36.5	15	2	US-09-239-043D-2101
4	27	36.5	15	2	US-09-239-043D-2101
5	27	36.5	15	2	US-09-239-043D-2101
6	27	36.5	15	2	US-09-239-043D-2101
7	27	36.5	15	2	US-09-239-043D-2101
8	27	36.5	15	2	US-09-239-043D-2101
9	27	36.5	15	2	US-09-239-043D-2101
10	27	36.5	15	2	US-09-239-043D-2101
11	27	36.5	15	2	US-09-239-043D-2101
12	27	36.5	15	2	US-09-239-043D-2101
13	27	36.5	15	2	US-09-239-043D-2101
14	27	36.5	15	2	US-09-239-043D-2101
15	27	36.5	15	2	US-09-239-043D-2101
16	27	36.5	15	2	US-09-239-043D-2101
17	27	36.5	15	2	US-09-239-043D-2101
18	27	36.5	15	2	US-09-239-043D-2101
19	27	36.5	15	2	US-09-239-043D-2101
20	27	36.5	15	2	US-09-239-043D-2101
21	27	36.5	15	2	US-09-239-043D-2101
22	27	36.5	15	2	US-09-239-043D-2101
23	27	36.5	15	2	US-09-239-043D-2101
24	27	36.5	15	2	US-09-239-043D-2101
25	27	36.5	15	2	US-09-239-043D-2101
26	27	36.5	15	2	US-09-239-043D-2101

27	24	32.4	15	2	US-09-060-872A-69	Sequence 69, App1
28	24	32.4	15	2	US-09-060-872A-70	Sequence 70, App1
29	24	32.4	15	2	US-09-060-872A-71	Sequence 71, App1
30	24	32.4	15	2	US-09-500-135C-69	Sequence 69, App1
31	24	32.4	15	2	US-09-500-135C-70	Sequence 70, App1
32	24	32.4	15	2	US-09-500-135C-71	Sequence 71, App1
33	24	32.4	15	2	US-09-500-135C-235	Sequence 235, App1
34	24	32.4	15	2	US-09-768-080-69	Sequence 69, App1
35	24	32.4	15	2	US-09-768-080-70	Sequence 70, App1
36	24	32.4	15	2	US-09-768-080-71	Sequence 71, App1
37	24	32.4	15	2	US-09-677-822A-69	Sequence 69, App1
38	24	32.4	15	2	US-09-677-822A-70	Sequence 70, App1
39	24	32.4	15	2	US-09-677-822A-71	Sequence 71, App1
40	24	32.4	15	2	US-09-677-822A-235	Sequence 235, App1
41	24	32.4	15	2	US-09-677-822A-264	Sequence 264, App1
42	23.5	31.8	15	2	US-09-009-953-264	Sequence 264, App1
43	23.5	31.8	15	2	US-09-239-043D-2188	Sequence 2188, App1
44	23	31.1	15	1	US-08-378-761A-50	Sequence 50, App1
45	23	31.1	15	1	US-08-485-286-50	Sequence 50, App1

ALIGNMENTS

RESULT 1
US-09-239-043D-2101
Sequence 2101, Application US/09239043D
Patent No. 6689363
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.006007
CURRENT APPLICATION NUMBER: US/09/239, 043D
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 09/189, 702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/978, 291
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820, 360
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 60/013, 363
PRIOR FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: US 08/461, 603
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/347, 610
PRIOR FILING DATE: 1994-12-01
PRIOR APPLICATION NUMBER: US 08/344, 824
PRIOR FILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278, 634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/205, 713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197, 484
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2101
LENGTH: 15
TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2101

Query Match 40.5%; Score 30; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GLNLSEPN 15
: |||:
Db 1 GTNLSPVN 8

RESULT 2
US-09-255-501-96
; Sequence 96, Application US/09255501
; Patent No. 6596525
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-96

Query Match 36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2,4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
: |||:
Db 5 ASLSLSG 12

RESULT 3
US-09-255-501-97
; Sequence 97, Application US/09255501
; Patent No. 6596525
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-97

Query Match 36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2,4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
: |||:
Db 2 ASLSLSG 9

RESULT 4
US-09-060-872A-96
; Sequence 96, Application US/09060872A
; Patent No. 6835550
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/060,872A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-060-872A-96

Query Match 36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2,4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
: |||:
Db 5 ASLSLSG 12

RESULT 5
US-09-060-872A-97
; Sequence 97, Application US/09060872A
; Patent No. 6835550
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/060,872A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-060-872A-97

Query Match 36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2,4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
: |||:
Db 2 ASLSLSG 9

RESULT 6
US-09-500-135C-96
; Sequence 96, Application US/09500135C
; Patent No. 6836269
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Harding, Fiona A.
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME

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FILE REFERENCE: A-68893/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/500,135C
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-500-135C-96

Query Match      36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 SKLSMSG 8
       : |||||
Db      5 ASLSLGS 12

RESULT 7
US-09-500-135C-97
; Sequence 97, Application US/09500135C
; Patent No. 6838269
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: A-68893/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/500,135C
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-500-135C-97

Query Match      36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 SKLSMSG 8
       : |||||
Db      2 ASLSLGS 9

RESULT 8
US-09-768-080-96
; Sequence 96, Application US/09768080
; Patent No. 6897049
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: GC527C3
; CURRENT APPLICATION NUMBER: US/09/768,080
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 09/677,822
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
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PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-768-080-96

Query Match      36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 SKLSMSG 8
       : |||||
Db      5 ASLSLGS 12

RESULT 9
US-09-768-080-97
; Sequence 97, Application US/09768080
; Patent No. 6897049
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: GC527C3
; CURRENT APPLICATION NUMBER: US/09/768,080
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 09/677,822
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-768-080-97

Query Match      36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 SKLSMSG 8
       : |||||
Db      2 ASLSLGS 9

RESULT 10
US-09-677-822A-96
; Sequence 96, Application US/09677822A
; Patent No. 6936249
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/09/677,822A
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
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; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-677-822A-96

Query Match
Best Local Similarity 36.5%; Score 27; DB 2; Length 15;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
DB 5 ASLSLGS 12

RESULT 11
US-09-677-822A-97
; Sequence 97, Application US/09677822A
; Patent No. 6936249
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: GCS27C2
; CURRENT APPLICATION NUMBER: US/09/677,822A
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-677-822A-97

Query Match
Best Local Similarity 36.5%; Score 27; DB 2; Length 15;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
DB 2 ASLSLGS 9

RESULT 12
US-08-572-951-6
; Sequence 6, Application US/08572951
; Patent No. 5824790
; GENERAL INFORMATION:
; APPLICANT: KEELING, PETER L.
; APPLICANT: KNIGHT, MARY E.
; APPLICANT: GUN, HANDING
; TITLE OF INVENTION: MODIFICATION OF STARCH
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: Pillsbury Madison & Sutro LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
```

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; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,951
; FILING DATE: 15-DEC-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,602
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/263,921
; FILING DATE: 21-JUN-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul N. Kokubis
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 222957/1.02.15C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-572-951-6

Query Match
Best Local Similarity 35.1%; Score 26; DB 1; Length 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GSGLN 10
DB 8 GSGLN 12

RESULT 13
US-08-572-951-23
; Sequence 23, Application US/08572951
; Patent No. 5824790
; GENERAL INFORMATION:
; APPLICANT: KEELING, PETER L.
; APPLICANT: KNIGHT, MARY E.
; APPLICANT: GUN, HANDING
; TITLE OF INVENTION: MODIFICATION OF STARCH
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: Pillsbury Madison & Sutro LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,951
; FILING DATE: 15-DEC-1995
; CLASSIFICATION: 800
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,602
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/263,921
; FILING DATE: 21-JUN-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul N. Kokulis
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 222957/1.02.15C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-572-951-23

Query Match      35.1%; Score 26; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GSGLN 10
      |||||
DB      8 GSGLN 12

RESULT 14
US-09-255-501-98
; Sequence 98, Application US/09255501
; Patent No. 6596525
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-98

Query Match      35.1%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LSMGSG 8
      |||||
DB      1 LSMGSG 6

RESULT 15
US-09-239-043D-2113
; Sequence 2113, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
```

```

; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2113
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2113

Query Match      35.1%; Score 26; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMGSLN 10
      |||||
DB      6 KIPMGVGLS 14
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Search completed: June 13, 2006, 02:48:37
Job time : 49 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 02:59:01 ; Search time 181 Seconds
(without alignments)
38.388 Million cell updates/sec

Title: US-10-612-162a-3
Perfect score: 74
Sequence: 1 SKLMSGGLNLSEPN 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 28443

Minimum DB seq length: 15
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celextra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /EMC_Celextra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_Celextra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_Celextra_SIDS3/prodata/2/pubppa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celextra_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celextra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	4	US-10-612-162-3 Sequence 3, Appli
2	55	74.3	15	5	US-10-769-514-10 Sequence 10, Appl
3	55	74.3	15	5	US-10-769-514-42 Sequence 42, Appl
4	55	74.3	15	5	US-10-801-990-180 Sequence 180, App
5	55	74.3	15	5	US-10-801-990-184 Sequence 184, App
6	30	40.5	15	5	US-10-654-601-184 Sequence 2101, Ap
7	28	37.8	15	5	US-10-769-514-16 Sequence 15, Appl
8	27	36.5	15	5	US-10-769-514-15 Sequence 15, Appl
9	27	36.5	15	5	US-10-924-082A-96 Sequence 96, Appl
10	27	36.5	15	5	US-10-924-092A-97 Sequence 97, Appl
11	27	36.5	15	5	US-10-895-064-574 Sequence 574, App
12	27	36.5	15	6	US-11-020-628-96 Sequence 96, Appl
13	27	36.5	15	6	US-11-020-628-97 Sequence 97, Appl
14	27	36.5	15	6	US-11-020-602-96 Sequence 96, Appl
15	27	36.5	15	6	US-11-020-602-97 Sequence 97, Appl
16	27	36.5	15	6	US-11-129-741-574 Sequence 574, App
17	26	35.1	15	4	US-10-149-138-3815 Sequence 3815, Ap
18	26	35.1	15	4	US-10-149-138-4460 Sequence 4460, Ap
19	26	35.1	15	4	US-10-149-138-3815 Sequence 3815, Ap
20	26	35.1	15	4	US-10-149-138-4460 Sequence 4460, Ap
21	26	35.1	15	5	US-10-495-146-87 Sequence 87, Appl
22	26	35.1	15	5	US-10-495-146-88 Sequence 88, Appl
23	26	35.1	15	5	US-10-495-146-89 Sequence 89, Appl
24	26	35.1	15	5	US-10-654-601-2113 Sequence 2113, Ap
25	26	35.1	15	5	US-10-654-601-2120 Sequence 2120, Ap
26	26	35.1	15	5	US-10-924-092A-98 Sequence 98, Appl
27	26	35.1	15	6	US-11-020-628-98 Sequence 98, Appl

28	26	35.1	15	6	US-11-084-080-120 Sequence 120, App
29	26	35.1	15	6	US-11-020-602-98 Sequence 98, Appl
30	25	33.8	15	3	US-09-908-943A-22 Sequence 22, Appl
31	25	33.8	15	4	US-10-149-137A-85 Sequence 85, Appl
32	25	33.8	15	4	US-10-149-137A-130 Sequence 130, App
33	25	33.8	15	4	US-10-149-137A-450 Sequence 450, App
34	25	33.8	15	5	US-10-801-487-22 Sequence 22, Appl
35	25	33.8	15	5	US-10-801-938-22 Sequence 22, Appl
36	25	33.8	15	5	US-10-801-509-22 Sequence 22, Appl
37	25	33.8	15	5	US-10-801-486-22 Sequence 22, Appl
38	25	33.8	15	5	US-10-801-486-22 Sequence 22, Appl
39	25	33.8	15	5	US-10-801-493-22 Sequence 22, Appl
40	24	32.4	15	4	US-10-206-699-92 Sequence 92, Appl
41	24	32.4	15	4	US-10-149-138-3820 Sequence 3820, Ap
42	24	32.4	15	4	US-10-149-138-3820 Sequence 3820, Ap
43	24	32.4	15	4	US-10-416-249-555 Sequence 555, App
44	24	32.4	15	4	US-10-149-137A-104 Sequence 104, App
45	24	32.4	15	4	US-10-475-104-42 Sequence 42, Appl

ALIGNMENTS

```
RESULT 1
US-10-612-162-3
Sequence 3, Application US/10612162
Publication No. US20040014145A1
GENERAL INFORMATION:
APPLICANT: Dade Behring Marburg GmbH
TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
FILE REFERENCE: 2002/B001
CURRENT APPLICATION NUMBER: US/10/612,162
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 10230550.1
PRIOR FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: 03011334.4
PRIOR FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-612-162-3

Query Match      100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY      1 SKLMSGGLNLSEPN 15
        |||
Db       1 SKLMSGGLNLSEPN 15

RESULT 2
US-10-769-514-10
Sequence 10, Application US/10769514
Publication No. US20040258695A1
GENERAL INFORMATION:
APPLICANT: Schreyers, Anthony
TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
FILE REFERENCE: 028722-001
CURRENT APPLICATION NUMBER: US/10/769,514
PRIOR FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US 60/444,113
PRIOR FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-769-514-10

Query Match 74.3%; Score 55; DB 5; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0091;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGINLSEPN 15
| | | | | | | | | | | | | | |
DB 1 LCMGSGINLCEPN 13

RESULT 3

US-10-769-514-42
; Sequence 42; Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schryver, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tbp-binding peptides
US-10-769-514-42

Query Match 74.3%; Score 55; DB 5; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0091;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGINLSEPN 15
| | | | | | | | | | | | | | |
DB 1 LCMGSGINLCEPN 13

RESULT 4

US-10-801-990-180
; Sequence 180; Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-180

Query Match 74.3%; Score 55; DB 5; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0091;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGINLSEPN 15
| | | | | | | | | | | | | | |
DB 1 LCMGSGINLCEPN 13

RESULT 5

US-10-801-990-184
; Sequence 184; Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-184

Query Match 74.3%; Score 55; DB 5; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0091;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGINLSEPN 15
| | | | | | | | | | | | | | |
DB 1 LCMGSGINLCEPN 13

RESULT 6

US-10-654-601-2101
; Sequence 2101; Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Bastejan
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chestnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2101
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-2101

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```

Query Match      40.5%; Score 30; DB 5; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      8 GLNLSEPN 15
Db      1 GTNLSPVN 8

```

```

RESULT 7
US-10-769-514-16
; Sequence 16, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schuyvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-10-769-514-16

```

```

Query Match      37.8%; Score 28; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      4 SMGSLNSEPN 15
Db      1 AMGYMALSKIN 12

```

```

RESULT 8
US-10-769-514-15
; Sequence 15, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schuyvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-10-769-514-15

```

```

Query Match      36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      5 MGSLNSEPN 15
Db      1 MGYGMAJSKIN 11

```

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RESULT 9
US-10-924-092A-96
; Sequence 96, Application US/10924092A
; Publication No. US20050137112A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN HUMANS AND
; FILE REFERENCE: GC527-1
; CURRENT APPLICATION NUMBER: US/10/924,092A
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-924-092A-96

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Query Match      36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 SKLSMSG 8
Db      5 ASLSLMSG 12

```

```

RESULT 10
US-10-924-092A-97
; Sequence 97, Application US/10924092A
; Publication No. US20050137112A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN HUMANS AND
; TITLE OF INVENTION: METHODS FOR CONSTRUCTING, IDENTIFYING AND PRODUCING SUCH PROTEIN
; FILE REFERENCE: GC527-1
; CURRENT APPLICATION NUMBER: US/10/924,092A
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-924-092A-97

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```

Query Match      36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      1 SKLSMSG 8
Db      2 ASLSLMSG 9

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```

RESULT 11
US-10-895-064-574
; Sequence 574, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.

```

APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
APPLICANT: CHAN, YI MAN
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN M.
APPLICANT: LEUNG, FREDERICK C.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
FILE REFERENCE: V0690.0031
CURRENT APPLICATION NUMBER: US/10/895,064
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: PatentIn version 3.2
SEQ ID NO 574
LENGTH: 15
TYPE: PRT
ORGANISM: Corononnavirus-HKU1
US-10-895-064-574

Query Match 36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 85.7%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 7
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Db 8 SKLSFGS 14

RESULT 12
US-11-020-628-96
Sequence 96, Application US/11020628
Publication No. US20050164257A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC527C2
CURRENT APPLICATION NUMBER: US/11/020,628
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 96
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-020-628-96

Query Match 36.5%; Score 27; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
: |||||
Db 5 ASLSLSG 12

RESULT 13
US-11-020-628-97
Sequence 97, Application US/11020628
Publication No. US20050164257A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC527C2

CURRENT APPLICATION NUMBER: US/11/020,628
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 97
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-020-628-97

Query Match 36.5%; Score 27; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
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Db 2 ASLSLSG 9

RESULT 14
US-11-020-602-96
Sequence 96, Application US/11020602
Publication No. US20060024764A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC527C2
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 96
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-020-602-96

Query Match 36.5%; Score 27; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
: |||||
Db 5 ASLSLSG 12

RESULT 15
US-11-020-602-97
Sequence 97, Application US/11020602
Publication No. US20060024764A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC527C2
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135

; PRIOR FILING DATE: 2000-02-08
 ; PRIOR APPLICATION NUMBER: US 09/060,872
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 240
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 97
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-11-020-602-97

Query Match 36.5%; Score 27; DB 6; Length 15;
 Best local Similarity 62.5%; Pred. No. 1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SKLSMSG 8
 :||:||||
 Db 2 ASLSLGS 9

Search completed: June 13, 2006, 03:02:14
 Job time : 181 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 02:59:21 ; Search time 17 Seconds
(without alignments)
11.156 Million cell updates/sec

Title: US-10-612-162a-3
Perfect score: 74
Sequence: 1 SKLWSGSLNSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 1754

Minimum DB seq length: 15
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New*

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- 3: /EMC_Celerra_SIDS3/pcodaca/2/pubppaa/US07_NEW_PUB.pap:*
- 4: /EMC_Celerra_SIDS3/pcodaca/2/pubppaa/US08_NEW_PUB.pap:*
- 5: /EMC_Celerra_SIDS3/pcodaca/2/pubppaa/PCT_NEW_PUB.pap:*
- 6: /EMC_Celerra_SIDS3/pcodaca/2/pubppaa/US10_NEW_PUB.pap:*
- 7: /EMC_Celerra_SIDS3/pcodaca/2/pubppaa/US11_NEW_PUB.pap:*
- 8: /EMC_Celerra_SIDS3/pcodaca/2/pubppaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	31.1	15	US-11-295-192A-1160	Sequence 1160, Ap
2	23	31.1	15	US-11-295-192A-1161	Sequence 1161, Ap
3	23	31.1	15	US-11-295-192A-1162	Sequence 1162, Ap
4	23	31.1	15	US-11-295-192A-1163	Sequence 1163, App
5	23	31.1	15	US-11-295-192A-1164	Sequence 1164, Ap
6	23	31.1	15	US-11-295-192A-1165	Sequence 1165, Ap
7	23	31.1	15	US-11-295-192A-1166	Sequence 1166, App
8	21	28.4	15	US-11-295-192A-232	Sequence 232, App
9	21	28.4	15	US-11-295-192A-233	Sequence 233, App
10	21	28.4	15	US-11-295-192A-234	Sequence 234, App
11	21	28.4	15	US-11-295-192A-235	Sequence 235, App
12	21	28.4	15	US-11-295-192A-236	Sequence 236, App
13	21	28.4	15	US-11-295-192A-237	Sequence 237, App
14	21	28.4	15	US-11-295-192A-238	Sequence 238, App
15	21	28.4	15	US-11-295-192A-239	Sequence 239, App
16	21	28.4	15	US-11-295-192A-1157	Sequence 1157, App
17	21	28.4	15	US-11-295-192A-1158	Sequence 1158, App
18	21	28.4	15	US-11-295-192A-1159	Sequence 1159, App
19	19	25.7	15	US-11-223-610-152	Sequence 152, App
20	19	25.7	15	US-11-295-192A-705	Sequence 705, App
21	19	25.7	15	US-11-295-192A-706	Sequence 706, App
22	19	25.7	15	US-11-295-192A-707	Sequence 707, App
23	19	25.7	15	US-11-295-192A-893	Sequence 893, App
24	19	25.7	15	US-11-295-192A-894	Sequence 894, App
25	19	25.7	15	US-11-295-192A-895	Sequence 895, App

26	19	25.7	15	7	US-11-295-192A-896	Sequence 896, App
27	19	25.7	15	7	US-11-295-192A-897	Sequence 897, App
28	19	25.7	15	7	US-11-295-192A-1167	Sequence 1167, App
29	19	25.7	15	7	US-11-263-230-263	Sequence 263, App
30	18	24.3	15	6	US-10-490-949-31	Sequence 31, App1
31	18	24.3	15	7	US-11-301-554-2116	Sequence 2116, App
32	18	24.3	15	7	US-11-140-487A-2148	Sequence 2148, App
33	18	24.3	15	7	US-11-140-487A-2150	Sequence 2150, App
34	18	24.3	15	7	US-11-140-487A-2217	Sequence 2217, App
35	18	24.3	15	7	US-11-295-192A-41	Sequence 41, App1
36	18	24.3	15	7	US-11-295-192A-42	Sequence 42, App1
37	18	24.3	15	7	US-11-295-192A-43	Sequence 43, App1
38	18	24.3	15	7	US-11-295-192A-44	Sequence 44, App1
39	18	24.3	15	7	US-11-295-192A-45	Sequence 45, App1
40	18	24.3	15	7	US-11-295-192A-46	Sequence 46, App1
41	18	24.3	15	7	US-11-295-192A-47	Sequence 47, App1
42	18	24.3	15	7	US-11-295-192A-48	Sequence 48, App1
43	18	24.3	15	7	US-11-295-192A-49	Sequence 49, App1
44	18	24.3	15	7	US-11-295-192A-800	Sequence 800, App
45	18	24.3	15	7	US-11-295-192A-801	Sequence 801, App

ALIGNMENTS

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RESULT 1
US-11-295-192A-1160
; Sequence 1160, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295, 192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1160
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1160
Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 SGLNLSSEPN 15
Db 7 SGINASVYN 15
RESULT 2
US-11-295-192A-1161
; Sequence 1161, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295, 192A
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;; CURRENT FILING DATE: 2005-12-06
;; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
;; PRIOR FILING DATE: 2004-06-14
;; NUMBER OF SEQ ID NOS: 1264
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1161
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1161

Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 SGNLSEPN 15
||:|:|
Db 6 SGINASVYN 14

RESULT 3
US-11-295-192A-1162
; Sequence 1162, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1162
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1162

Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 SGNLSEPN 15
||:|:|
Db 5 SGINASVYN 13

RESULT 4
US-11-295-192A-1163
; Sequence 1163, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14

;; NUMBER OF SEQ ID NOS: 1264
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1163
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1163

Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 SGNLSEPN 15
||:|:|
Db 4 SGINASVYN 12

RESULT 5
US-11-295-192A-1164
; Sequence 1164, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1164
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1164

Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 SGNLSEPN 15
||:|:|
Db 3 SGINASVYN 11

RESULT 6
US-11-295-192A-1165
; Sequence 1165, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1165

LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1165

Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 SGNLSEPN 15
Db 2 SGINASVYN 10

RESULT 7
US-11-295-192A-1166

Sequence 1166, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Wouter C.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295.192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1166
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-1166

Query Match 31.1%; Score 23; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 SGNLSEPN 15
Db 1 SGINASVYN 9

RESULT 8

US-11-295-192A-232
Sequence 232, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Wouter C.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295.192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 232
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence

FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-232

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 SGNLSEPN 14
Db 8 SGFNTLKP 15

RESULT 9

US-11-295-192A-233
Sequence 233, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Wouter C.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295.192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 233
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-233

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 SGNLSEPN 14
Db 7 SGFNTLKP 14

RESULT 10

US-11-295-192A-234
Sequence 234, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Wouter C.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295.192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 234
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-234

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 SGNLSEP 14
DB 6 SGFNLTLP 13

RESULT 11

US-11-295-192A-235
; Sequence 235, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 235
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-235

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 SGNLSEP 14
DB 5 SGFNLTLP 12

RESULT 12

US-11-295-192A-236
; Sequence 236, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 236
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-236

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 SGNLSEP 14
DB 4 SGFNLTLP 11

RESULT 13

US-11-295-192A-237
; Sequence 237, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 237
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-237

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 SGNLSEP 14
DB 3 SGFNLTLP 10

RESULT 14

US-11-295-192A-238
; Sequence 238, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 238
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-238

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 SGNLSEP 14

Db 2 SCFNITLKP 9

```

RESULT 15
US-11-295-192A-239
; Sequence 239, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Siooestra, Jelle W.
; APPLICANT: Pulik, Mouter C.
; APPLICANT: Goudemits, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-239

```

```

Query Match 28.4%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 SGINTLSEP 14
Db 1 SCFNITLKP 8

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Search completed: June 13, 2006, 03:02:36
Job time : 17 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 03:50:08 ; Search time 84.1176 Seconds
(without alignments)
70.661 Million cell updates/sec

Title: US-10-612-162A-4

Perfect score: 68
Sequence: 1 YEKYLGEHYKAV 13Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	ADG46078	Adg46078 Human CDT
2	68	100.0	49	ABP72836	Abp72836 Human tra
3	68	100.0	49	ADH89394	Adh89394 Human tra
4	68	100.0	49	ADK15882	Adk15882 Human tra
5	68	100.0	49	ADL70756	Adl70756 Human tra
6	68	100.0	137	ADF74798	Adf74798 Human NOV
7	68	100.0	328	AAH84371	Aah84371 Amino aci
8	68	100.0	539	AAU02980	Aau02980 Angiotens
9	68	100.0	575	ABR82321	Abm82321 Human met
10	68	100.0	609	ABM83782	Abm83782 Human dia
11	68	100.0	627	ABM83781	Abm83781 Human dia
12	68	100.0	628	ABM83779	Abm83779 Human dia
13	68	100.0	635	ADT08174	Adt08174 Human met
14	68	100.0	643	ABM83778	Abm83778 Human dia
15	68	100.0	645	ABM83783	Abm83783 Human dia
16	68	100.0	646	AAU02938	Aau02938 Angiotens
17	68	100.0	645	ABM83780	Abm83780 Human dia
18	68	100.0	679	ABP72820	Abp72820 Human tra
19	68	100.0	679	ADH89360	Adh89360 Human tra
20	68	100.0	679	ADK15869	Adk15869 Mature hu
21	68	100.0	679	ADL70732	Adl70732 Human tra
22	68	100.0	679	ADL24413	Adl24413 Human tra
23	68	100.0	679	ADU17885	Adu17885 Human tra

24	68	100.0	679	8	ADT55264	Adt55264 Partial h
25	68	100.0	679	8	ADU07204	Adu07204 Amino aci
26	68	100.0	679	8	ADT78912	Adt78912 Human tra
27	68	100.0	679	8	ADT78149	Adt78149 Human tra
28	68	100.0	679	8	ADT99248	Adt99248 Partial h
29	68	100.0	679	8	ADT36538	Adt36538 Partial h
30	68	100.0	679	8	ADT98423	Adt98423 Human tra
31	68	100.0	679	8	ADU17611	Adu17611 Human tra
32	68	100.0	679	8	ADU17468	Adu17468 Human tra
33	68	100.0	679	8	ADU00630	Adu00630 Human tra
34	68	100.0	679	8	ADT55066	Adt55066 Human par
35	68	100.0	679	9	ADY54149	Ady54149 Amino aci
36	68	100.0	679	9	ADY57102	Ady57102 Human ser
37	68	100.0	679	9	ADY57103	Ady57103 Human ser
38	68	100.0	679	10	ABE47501	Abe47501 Human tra
39	68	100.0	696	1	AAE70384	Aae70384 Sequence
40	68	100.0	698	2	AAE12499	Aae12499 Human tra
41	68	100.0	698	2	AAE6492	Aae6492 Human tra
42	68	100.0	698	2	AAW54354	Aaw54354 Serotrans
43	68	100.0	698	3	AAV50717	Aav50717 Human tra
44	68	100.0	698	6	ABP72819	Abp72819 Human tra
45	68	100.0	698	7	ADD45282	Add45282 Human pro

ALIGNMENTS

RESULT 1
ID ADG46078 standard; peptide; 13 AA.
XX
AC ADG46078;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #4.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KW non-glycosylated transferrin; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN EP378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PS (DADE-) DADE BEHRING WARBURG GMBH.
XX
PI Alphas H;
XX
WP: 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
XX need for immobilization.
XX
PS Claim 4; SEQ ID NO 4; 21pp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequences VVARSMGSGKEDLWELL, TTEDSIKIMNGEADMSIDGGF, SKLSMGSGLNSBN and
CC YEKYLGEHYKAV (ADG46078-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention.
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for

CC production of antibodies that specifically bind CDR from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC acetalcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 68; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
 |||||
 DB 1 YEKYLGEYVKAV 13

RESULT 2

ABP72836
 ID ABP72836 standard; peptide; 49 AA.

XX ABP72836;

DT 11-AUG-2003 (first entry)

DE Human transferrin peptide insertion region.

XX Transferrin; neuroprotective; cerebroprotective; vasotropic;
 XX antiParkinsonian; nootropic; anti-HIV; antiaesthetic; antiallergic;
 XX cytotatic; immunosuppressive; antithrombotic; cardiac;
 XX gynaecological; immunostimulant; antinaemic; haemostatic;
 XX antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
 XX fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;
 XX tranquilizer; vulnerary; antidiabetic; nephrotoxic; antipyretic;
 KM gastrointestinal; gene therapy; transgenic animal.

XX Homo sapiens.

OS Homo sapiens.

FN Modified-site 1. .3 Location/Qualifiers

FT /note="Asn is N-glycosylated"

FT Misc-difference 15.16 "peptide insertion site"

PN WO2003020746-A1.

PD 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027637.

XX 30-AUG-2001; 2001US-0315745P.

PR 30-NOV-2001; 2001US-0334059P.

XX (BIOR-) BIOREXIS PHARM CORP.

PI Prior CP;

DR WPI; 2003-332916/31.

PT New fusion protein, useful in the diagnosis and treatment of diseases or

PS disorders relating to a transferrin protein fused to a therapeutic protein.

XX Example 3; Page 249; 298pp; English.

CC The present sequence is a portion of the human transferrin (Tf) C domain,
 CC comprising amino acids 611-659 of the Tf sequence given in ABP72820. The
 CC invention relates to novel fusion proteins of Tf and a therapeutic
 CC protein or peptide. The therapeutic protein or peptide, e.g. an
 CC erythropoietin mimetic (see ABP72834), can be fused to the N- or C-
 CC termini of Tf, or inserted into Tf especially between residues Glu-625

CC and Thr-626 of the Tf N domain. Modified Tf fusion proteins of the
 CC invention can be used in the diagnosis, prognosis, prevention and/or
 CC treatment of diseases and/or disorders of the endocrine, nervous, immune,
 CC respiratory, cardiovascular, reproductive and digestive systems, diseases
 CC and/or disorders relating to the blood or to cell proliferation,
 CC inflammatory conditions and infectious diseases, or to deliver a
 CC therapeutic agent to a cell or across the blood-brain barrier

XX Sequence 49 AA;

Query Match 100.0%; Score 68; DB 6; Length 49;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
 |||||
 DB 37 YEKYLGEYVKAV 49

RESULT 3

ADH89394
 ID ADH89394 standard; protein; 49 AA.

XX ADH89394;

DT 15-APR-2004 (first entry)

DE Human transferrin protein domain SegID38.

XX fusion protein; transferrin protein; glycosylation;
 XX antibody variable region; cytostatic; antibacterial; virucide;
 KM antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 KM septic shock; endotoxemic shock; cachexia syndrome; bacterial infection;
 KM viral infection; parasitic infection; neoplasm; autoimmune disease;
 XX arthritis; graft rejection; human.

XX Homo sapiens.

PN US2003226155-A1.

PD 04-DEC-2003.

PF 10-MAR-2003; 2003US-00384060.

PR 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0334059P.

PR 30-AUG-2002; 2002US-0406977P.

XX (BIOR-) BIOREXIS PHARM CORP.

PI Sadeghi H, Prior CP, Turner A;

DR WPI; 2004-022093/02.

PT New fusion protein comprising a transferrin protein exhibiting reduced

PS glycosylation fused to at least one antibody variable region, useful for

XX preparing a composition for treating e.g., septic shock, neoplasm or

XX autoimmune disease.

XX Example 2; SEQ ID NO 38; 82pp; English.

CC This invention relates to a novel fusion protein which comprises a
 CC transferrin protein exhibiting reduced glycosylation fused to at least
 CC one antibody variable region. The invention may be useful for the
 CC development of compounds with cytostatic, antibacterial, virucide,
 CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
 CC the sequences disclosed may be useful for gene therapy. The fusion
 CC protein is useful for preparing a composition for treating a disease or
 CC disease symptom in a patient for example septic shock, endotoxemic shock,
 CC cachexia syndromes associated with bacterial, viral or parasitic
 CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
 CC associated with treatment for preventing graft rejection. The present

SQ Sequence 49 AA:

Query Match 100.0%; Score 68; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
13 YEKYLGEYVKAV 49

Db 37 YEKYLGEYVKAV 49

RESULT 6
ADP74798
ID ADF74798 standard; protein; 137 AA.
XX
XX ADF74798;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Human NOVX protein to treat human pathological conditions (SeqID 12).
DE
XX
XX human; NOVX; metabolic disorder; diabetes; anorexia; cancer;
KM cardiovascular; infectious; neurodegenerative; immune;
KM haematopoietic disease; dyslipidaemia; anorectic; vitruclide; nootropic;
KM antiinflammatory; neuroprotective; antilipemic; anabolic; cardiant;
KM neurogenesis; wound healing; angiogenesis; chromosome mapping;
KM tissue typing; preventive medicine; pharmacogenomic.
XX
XX Homo sapiens.
OS
XX
XX WO2003076578-A2.
PN
XX
XX 18-SEP-2003.
PD
XX
XX 06-MAR-2003; 2003WO-US006794.
PF
XX
XX 06-MAR-2002; 2002US-0361974P.
PR 08-MAR-2002; 2002US-00093463.
PR 08-MAR-2002; 2002WO-US007288.
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 20-MAR-2002; 2002US-0365884P.
PR 20-MAR-2002; 2002US-0365984P.
PR 20-MAR-2002; 2002US-0365985P.
PR 22-MAR-2002; 2002US-036628P.
PR 12-APR-2002; 2002US-0372018P.
PR 12-APR-2002; 2002US-0372022P.
PR 23-APR-2002; 2002US-0374682P.
PR 12-JUN-2002; 2002US-0388096P.
PR 14-JUN-2002; 2002US-0389143P.
PR 26-JUN-2002; 2002US-0391779P.
PR 15-AUG-2002; 2002US-0403743P.
PR 13-SEP-2002; 2002US-0410755P.
PR 23-SEP-2002; 2002US-0412957P.
PR 22-OCT-2002; 2002US-0420382P.
PR 05-MAR-2003; 2003US-00420382.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX AIsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;
PI Colman SD, Edinger SR, Ettenberg S, Gangoli EA, Gerlach VL;
PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malpankar UM;
PI Mezer PS, Miller CE, Miller I, Padigaru M, Patnirajan M, Peyman J;
PI Qian X, Rastelli L, Rieger DK, Smithson G, Szytek KA, Stone DJ;
PI Sukumaran S, Vernet CAM, Voss EZ, Zhong M;
XX
XX WPI; 2003-697890/66.
DR N-PSDB; ADF74797.
XX
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.

XX
PS Claim 1; SEQ ID NO 12; 282pp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating metabolic disorders, diabetes,
CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
CC and haematopoietic diseases as well as various dyslipidaemias.
CC Accordingly, these molecules have many activities including anorectic,
CC vitruclide, nootropic, antiinflammatory, neuroprotective, antilipemic,
CC anabolic and cardiant. Furthermore, they are useful in screening assays
CC to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
XX
SQ Sequence 137 AA:

Query Match 100.0%; Score 68; DB 7; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
105 YEKYLGEYVKAV 117

Db 105 YEKYLGEYVKAV 117

RESULT 7
AAB84371
ID AAB84371 standard; protein; 328 AA.
XX
XX AAB84371;
AC
XX
XX 22-AUG-2001 (first entry)
DT
XX
XX Amino acid sequence of a human transferrin.
DE
XX
XX Human; transferrin; autoimmune disease; rheumatoid arthritis;
KM hyperproliferative disorder; neoplasm; cardiovascular disorder;
KM cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KM ocular disorder; corneal infection; wound healing;
KM epithelial cell proliferation; aging; organ transplant.
XX
XX Homo sapiens.
OS
XX
XX WO200146254-A1.
PN
XX
XX 28-JUN-2001.
PD
XX
XX 21-DEC-2000; 2000WO-US034769.
PF
XX
XX 23-DEC-1999; 99US-0171595P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Shi Y, Choi GH;
PI
XX
XX WPI; 2001-381910/40.
DR N-PSDB; AAB25190.
XX
XX
XX Isolated nucleic acid molecule encoding a human transferrin protein is
PT used in preventing, treating or ameliorating a medical condition.
PT
XX Claim 11; Page 286-287; 290pp; English.

XX The present sequence represents human transferrin polypeptide.
CC Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities
XX

CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis
XX

SO Sequence 328 AA:
Query Match 100.0%; Score 68; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SO Sequence 539 AA:
Query Match 100.0%; Score 68; DB 4; Length 539;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGEYVAV 13
Db 296 YEKYLGEYVAV 308

Qy 1 YEKYLGEYVAV 13
Db 507 YEKYLGEYVAV 519

RESULT 8
AAU02980
ID AAU02980 standard; protein; 539 AA.

RESULT 9
ABR82321
ID ABR82321 standard; protein; 575 AA.

AC AAU02980;
DT 12-SEP-2001 (first entry)

AC ABR82321;
DT 06-NOV-2003 (first entry)

XX Angiotensin converting enzyme (ACEV) splice variant protein #80.

DE Human metalloprotein (MEPR) polypeptide (Id=7509328CD1).

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardiial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

XX MEPR; metalloprotein; anti-HIV; antiallergic; antiinflammatory; human;
KW antianemic; antiparkinsonian; nootropic; anticonvulsant; cytostatic;
KW antidiabetic; antiaschemic; immunosuppressive; antithyroid;
KW hepatotropic; dermatological; antidiabetic; nephrotropic; antiouf;
KW thyromimetic; neuroprotective; osteopathic; antiarthritic; uropathic;
KW antiparasitic; antihelminthic; antiparasitic; ophthalmological; virucide;
KW antineumatic; haemostatic; antibacterial; protozoacide; fungicide;
KW gene therapy; transgenic.

XX Homo sapiens.
OS
XX
XX WO20013632-A2.

XX Homo sapiens.
OS
XX
XX WO2003060089-A2.

XX 25-MAY-2001.

XX 14-JAN-2003; 2003WO-US001485.

XX 17-NOV-2000; 2000WO-IL000766.

XX 14-JAN-2002; 2002US-0348769P.

XX 17-NOV-1999; 99IL-00132978.

XX 18-JAN-2002; 2002US-0350701P.

XX 10-DEC-1999; 99IL-00133455.

XX 19-MAR-2002; 2002US-036059P.

XX (COMP-) COMPUGEN LTD.

XX (INCY-) INCYTE GENOMICS INC.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
PI WPI; 2001-336004/35.

PI Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW;
PI Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Marquis JP;

XX N-PSDB; AAS06080.

XX WPI; 2003-598523/56.

XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

PT New human metalloproteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
PT hepatitis.

PS Claim 4; Fig 80; 519pp; English.

XX PS Claim 1, Page 146-148; 153pp; English.
XX CC The invention relates to novel human metalloproteins (MEPR) and encoding
XX CC polynucleotides. The human MEPR polypeptides, polynucleotides and
XX CC modulators are useful for diagnosing, treating or preventing disorders
XX CC associated with aberrant expression of MEPR, particularly cell
XX CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
XX CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
XX CC vera, porphyria, primary thrombocytopenia or cancer), developmental
XX CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
XX CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
XX CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
XX CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
XX CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
XX CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
XX CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
XX CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
XX CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
XX CC polynucleotides encoding MEPR are useful for creating transgenic animals
XX CC to model human disease. Sequences ABR82316-323 represent the human MEPR
XX CC polypeptides of the invention
XX SQ Sequence 575 AA:

Query Match 100.0%; Score 68; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
|||
543 YEKYLGEYVKAV 555

Db 543 YEKYLGEYVKAV 555

RESULT 10
ABM83782
ID ABM83782 standard; protein; 609 AA.
XX AC ABM83782;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4031.
XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
XX PI Harthshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV,
XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kitron ES;
XX PI Xu Y, Kwong M, Policky JL, Hurlwitz BL, Ma Y, Jackson JL, Gietzen D;
XX PI Patuty S, Shi X, Suarez CJ;
XX DR WPI; 2004-329368/30.
XX DR N-PDB; ACN42434.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX PS Claim 27, Page; 190pp; English.
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
XX CC selected from one of the 2722 sequences defined in the specification. A
XX CC polynucleotide of the invention may have a use in gene therapy. The human
XX CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
XX CC used to diagnose a particular condition, disease or disorder associated
XX CC with human molecules, e.g. cell proliferative disorder,
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine
XX CC disorder, neurological disorder, gastrointestinal disorders, or
XX CC infections caused by virus, bacteria, fungi or parasite. The dthp
XX CC molecules may also be used in genetic mapping, in identifying individuals
XX CC from minute biological samples, in detecting single nucleotide
XX CC polymorphisms, as molecular weight markers, and for somatic or germ-line
XX CC gene therapy. The present sequence represents a dthp protein of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ Sequence 609 AA:

Query Match 100.0%; Score 68; DB 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
|||
577 YEKYLGEYVKAV 589

Db 577 YEKYLGEYVKAV 589

RESULT 11
ABM83781
ID ABM83781 standard; protein; 627 AA.
XX AC ABM83781;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.
XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
XX PI Harthshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV,
XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kitron ES;
XX PI Xu Y, Kwong M, Policky JL, Hurlwitz BL, Ma Y, Jackson JL, Gietzen D;
XX PI Patuty S, Shi X, Suarez CJ;
XX DR WPI; 2004-329368/30.
XX DR N-PDB; ACN42433.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorder, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 627 AA;
XX
Query Match 100.0%; Score 68; DB 8; Length 627;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 YEKYLGEYVYKAV 13
|||
595 YEKYLGEYVYKAV 607
XX
Db
XX
RESULT 12
ABM83779
ID ABM83779 standard; protein; 628 AA.
XX
XX ABM83779;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4028.
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorn TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Barville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Parralra CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vite UA, Kirtson ES;
PI Xu Y, Krong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX
XX N-PSDB; ACN42431.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorder, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 628 AA;
XX
Query Match 100.0%; Score 68; DB 8; Length 628;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 YEKYLGEYVYKAV 13
|||
596 YEKYLGEYVYKAV 608
XX
Db
XX
RESULT 13
ADT08174
ID ADT08174 standard; protein; 635 AA.
XX
XX ADT08174;
XX
XX 30-DEC-2004 (first entry)
XX
XX Human metal binding protein (MBP) (ID: 7512697CD1).
XX
XX MBP; metal binding protein; cytosolic; antiarteriosclerotic;
XX anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV;
XX antiallergic; antiinflammatory; thyromimetic; transgenic; human.
XX
XX Homo sapiens.
XX
XX WO2004085612-A2.
XX
XX 07-OCT-2004.
XX
XX 17-MAR-2004; 2004WO-US008328.
XX
XX 24-MAR-2003; 2003US-0457538P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Jiang X, Jackson AA, Hafalia AJA, Mason PM;
PI WPI; 2004-710307/69.
XX
XX N-PSDB; ADT08177.
XX
XX New human metal binding proteins (MBP), useful for diagnosing, treating
PT and preventing diseases or conditions associated with the aberrant MBP
PT expression e.g. cancer, AIDS, epilepsy, or infections.
XX
XX Claim 1, SEQ ID NO 3, 161pp; English.
XX
XX The invention relates to novel human metal binding proteins (MBP) and
CC encoding polynucleotides. The MBPs can be expressed by standard
CC recombinant methodology. The polypeptides and polynucleotides are useful
CC in diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of MBP, such as cell

CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX

SQ Sequence 645 AA;

Query Match 100.0%; Score 68; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
|||
Db 613 YEKYLGEYVKAV 625

Search completed: June 13, 2006, 03:58:16
Job time : 86.1176 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:18:14 ; Search time 13.1912 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-4
Sequence: 1 YEKYLGEERYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR:80:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	68	100.0	698	1	TFHUP
2	58	85.3	694	1	TFRBP
3	56	82.4	703	2	A45543
4	55	80.9	708	2	JC2133
5	51	75.0	695	2	S49163
6	51	75.0	704	2	I47228
7	48	70.6	708	1	TFBOL
8	48	70.6	215	2	A60166
9	48	70.6	216	1	A39684
10	48	70.6	711	1	TFHUR
11	47	69.1	696	1	S01384
12	45	66.2	706	2	S33761
13	45	66.2	707	1	A28438
14	44	64.7	305	2	D64326
15	43	63.2	334	2	E75153
16	43	63.2	614	2	B83818
17	43	63.2	692	2	H70362
18	42	61.8	115	2	T50390
19	42	61.8	188	2	D64017
20	41	60.3	408	2	H97236
21	41	60.3	431	2	C86812
22	41	60.3	500	2	B98852
23	41	60.3	711	2	S37025
24	40	58.8	203	2	T39117
25	40	58.8	425	2	A99939
26	40	58.8	466	1	SYECNT
27	40	58.8	466	2	AF0616
28	40	58.8	466	2	C85619
29	40	58.8	466	2	B90755

30	40	58.8	467	2	B96829	probable sugar tra
31	40	58.8	518	1	XYIMA	homoserine O-acety
32	40	58.8	635	2	A42968	dnak-type molecule
33	40	58.8	738	1	TFHUM	melanotransferrin
34	39.5	57.4	328	1	B64478	hypothetical prote
35	39	57.4	311	2	A28446	transferrin - mous
36	39	57.4	334	1	DEQY	glyceraldehyde-3-p
37	39	57.4	407	2	E70309	hypothetical prote
38	39	57.4	600	2	A49230	dnak-type molecule
39	39	57.4	605	2	I39837	dnak-type molecule
40	39	57.4	607	2	B50060	dnak protein limpo
41	39	57.4	607	2	G97928	hypothetical prote
42	39	57.4	661	2	A69252	3-hydroxyacyl-CoA
43	39	57.4	728	2	S59664	procollagen-lysine
44	39	57.4	731	2	D71332	probable DNA topoi
45	39	57.4	883	2	T06848	phycobillosome link

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor [validated] - human
N/Alternate names: siderophilin
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1982 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
C/Accession: A20981; A92417; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A03
R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bregt, P.H.; Baldwin
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A/Title: Human transferrin: cDNA characterization and chromosomal localization.
A/Reference number: A20981; MUID:84194084; PMID:6585826
A/Contents: variant C
A/Accession: A20981
A/Molecule type: mRNA
A/Residues: 1-698 <YAN>
A/Cross-references: UNIPROT:P02787, UNIPARC:UPI000002F089; EMBL:M12530; NID:g339452; PIDN:
A/Note: The authors translated the codon CAA for residue 203 as Glu
R/MacGillivray, R.T.A.; Mendez, E.; Stewale, J.G.; Sinha, S.K.; Lineback-Zins, J.; Brew,
J. Biol. Chem. 259, 3543-3553, 1983
A/Title: The primary structure of human serum transferrin. The structures of seven cyano
A/Reference number: A92417; MUID:83160878; PMID:6833213
A/Accession: A92417
A/Molecule type: protein
A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-
A/Cross-references: UNIPARC:UPI0000174483
A/Note: the sequence shown is the predominant electrophoretic genetic variant (C or TFC)
R/Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A/Title: Organization of the human transferrin gene: direct evidence that it originated b
A/Reference number: A94044; MUID:85216459; PMID:3858812
A/Accession: A94044
A/Molecule type: DNA
A/Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A/Cross-references: UNIPARC:UPI0000174484; EMBL:M11361
R/Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A/Title: The human transferrin gene: 5' region contains conserved sequences which match t
A/Reference number: A29090; MUID:87192006; PMID:3106157
A/Accession: A29090
A/Molecule type: DNA
A/Residues: 1-72, 291-300 <ADR>
A/Cross-references: UNIPARC:UPI000016B0AC; UNIPARC:UPI000016B0AD; EMBL:M15673
R/Uzun, G.; Fraim, M.; Park, I.; Besmond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; Kal
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A/Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A/Reference number: A32739; MUID:84135910; PMID:6322780
A/Accession: A32739
A/Molecule type: mRNA
A/Residues: 422-690, 'G', 692-698 <UZA>
A/Cross-references: UNIPARC:UPI000016B0AB; EMBL:M15251; NID:g339468; PIDN:AAA61142.1; PIR
R/MacGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew,

Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A/Title: The complete amino acid sequence of human serum transferrin.

A/Reference number: A93911; MUID:8222216; PMID:6953407

A/Contents: annotation; disulfide bonds

R/Author: C.L. Larson, J.L. Arnold, B. Roseck, P.R. Ann. N. Y. Acad. Sci. 646, 140-154, 1991

A/Title: A cloned gene for human transferrin.

A/Reference number: IS1959; MUID:9223339; PMID:1809186

A/Accession: IS1959

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-698 <RES>

A/Cross-references: UNIPARC:UPI00002089; GB:695936; NID:9248647; PIDN:AAH22049.1; PID: R/buguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.

Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989

A/Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.

A/Reference number: I48174; MUID:89386721; PMID:2780570

A/Accession: I63133

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 636-696 <RE2>

A/Cross-references: UNIPARC:UPI000016B13C; GB:M26641; NID:9339988; PIDN:AAA61233.1; PID: R/Schaeffer, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.J.; Champion, P.; Cohen, Gene 56, 109-116, 1987

A/Title: Complete structure of the human transferrin gene. Comparison with analogous chi

A/Reference number: I54011; MUID:8805305; PMID:3678832

A/Accession: I54011

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-72 <RE3>

A/Cross-references: UNIPARC:UPI000016B0AC; GB:M17611; NID:9339480; PIDN:AAA61147.1; PID: A/Accession: I68160

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 564-698 <RE4>

A/Cross-references: UNIPARC:UPI000016B0AE; GB:M17614; NID:9339483; PIDN:AAA61148.1; PID: C/Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion

C/Genetics:

A/Gene: GDB:TF

A/Cross-references: GDB:120432; OMIM:190000

A/Map position: 3q21-3q21

A/Intons: 15/1; 72/3; 119/1; 168/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49

C/Function:

A/Description: binds iron for delivery into cells

C/Superfamily: transferrin; transferrin repeat homology

C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-698/Product: transferrin #status experimental <MAT>

F/20-350/Domain: transferrin repeat homology <TRH1>

F/356-686/Domain: transferrin repeat homology <TRH2>

F/38-67;38-58;137-213;156-350;177-193;180-196;190-198;246-260;358-615;364-396;374-387;42

F/432;630/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 68; DB 1; Length 698;

Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERYLGEYKAV 13

Db 666 YERYLGEYKAV 678

RESULT 2

TFRBP

transferrin precursor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1993 #sequence revision 1993 #text change 22-Jun-1999

C/Accession: S16246; A61233; S00335; S02694; A26504; S14853

R/Author: D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umelae, T.M.; Woodworth, R. Biochim. Biophys. Acta 1089, 262-265, 1991

A/Title: The nucleotide sequence of rabbit liver transferrin cDNA.

A/Reference number: S16246; MUID:91274362; PMID:2054387

A/Accession: S16246

A/Molecule type: mRNA

A/Residues: 1-694 <BAN>

A/Cross-references: UNIPARC:UPI000016C5CE; EMBL:X58533; NID:91750; PIDN:CAA41424.1; PID: R/Pierpoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J. Cell. Immunol. 134, 225-234, 1991

A/Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and endu

A/Reference number: A61339; MUID:91191584; PMID:2013104

A/Accession: A61339

A/Molecule type: protein

A/Residues: 19-36 <PIE>

A/Cross-references: UNIPARC:UPI00001744A6

R/Author: M.C.M.; Chan, S.L.; Shimizu, S. Int. J. Biochem. 23, 609-616, 1991

A/Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.

A/Reference number: A61573; MUID:91293379; PMID:2065820

A/Accession: C61573

A/Molecule type: protein

A/Residues: 19-26; 'X', 28-36; 'X', 38-53 <CHU>

R/Author: Godovac-Zimmermann, J. Biol. Chem. Hoppe-Seyler 369, 93-96, 1988

A/Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf

A/Reference number: S00335; MUID:88209278; PMID:3365331

A/Accession: S00335

A/Molecule type: protein

A/Residues: 19-45; 'S', 47-48; 'Y', 50 <GOD>

A/Cross-references: UNIPARC:UPI00001744A8

R/Author: Evans, R.W.; Altken, A.; Patel, K.J. FEBS Lett. 238, 39-42, 1988

A/Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of

A/Reference number: S02694; MUID:89005676; PMID:3169252

A/Accession: S02694

A/Molecule type: protein

A/Residues: 482-515; 'V', 517-544 <EVA>

A/Cross-references: UNIPARC:UPI00001744A9

A/Note: 516-Ile was also found

R/Author: Heaphy, S.; Williams, J. Biochem. J. 205, 611-617, 1982

A/Title: The preparation and partial characterization of N-terminal and C-terminal iron-t

A/Reference number: A26504; MUID:83074540; PMID:6816218

A/Accession: A26504

A/Molecule type: protein

A/Residues: 19-24; 'N', 26; 'X', 28-29; 'S', <HEA>

A/Cross-references: UNIPARC:UPI00001744AA

C/Superfamily: transferrin; transferrin repeat homology

C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-694/Product: transferrin #status experimental <MAT>

F/19-349/Domain: transferrin repeat homology <TRH1>

F/355-682/Domain: transferrin repeat homology <TRH2>

F/22-66;37-57;136-212;155-349;176-192;179-195;189-197;245-259;357-611;363-395;373-386;42

F/508/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 85.3%; Score 58; DB 1; Length 694;

Best Local Similarity 76.9%; Pred. No. 0.063;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YERYLGEYKAV 13

Db 662 YERYLGEYKAV 674

RESULT 3

A45543

lactoferrin precursor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text change 09-Jul-2004

C/Accession: A45543; S24173

R/Author: Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W. Ann. Genet. 23, 251-256, 1992

A/Title: Cloning and sequencing of the porcine lactoferrin cDNA.

A/Reference number: A45543; MUID:92367939; PMID:1503259

A/Accession: A45543

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-703 <ALE>
 A:Cross-references: UNIPROT:P14632; UNIPARC:UPI0000177C55
 A:Experimental source: mammary gland
 A>Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBI:P.111153)
 R:Lydon, J.P.; O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Comeely, O.M.
 Biochim. Biophys. Acta 1132, 97-99, 1992
 A:Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A:Reference number: S24173; MUID:92379101; PMID:1511016
 A:Accession: S24173
 A:Molecule type: mRNA
 A:Residues: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
 A:Cross-references: UNIPARC:UPI000016C6E2; EMBL:M92089; NID:G164613; PIDN:AAA31102.1; PI
 A:Experimental source: mammary gland
 A:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-703/Product: lactoferrin #status predicted <MAT>
 F:20-350/Domain: transferrin repeat homology <TRH1>
 F:36-48/Region: antimicrobial
 F:354-691/Domain: transferrin repeat homology <TRH2>
 F:28-62,38-53,129-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,45
 F:77,107,206,267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:135/Binding site: carbonate (Arg) #status predicted
 F:409,447,540,609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Arg) #status predicted
 F:490/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.4%; Score 56; DB 2; Length 703;
 Best Local Similarity 76.9%; Pred. No. 0.14;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
 |||||
 Db 671 YEKYLGEYVAV 683

RESULT 4
 JC2323
 Lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JC2323
 R:Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A:Reference number: JC2323; MUID:94380047; PMID:8093048
 A:Accession: JC2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 A:Cross-references: UNIPARC:UPI0000177C50
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-596/Domain: transferrin repeat homology <TRH2>
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.9%; Score 55; DB 2; Length 708;
 Best Local Similarity 76.9%; Pred. No. 0.21;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
 |||||
 Db 676 YEKYLGEYVAV 688

RESULT 5
 S49163
 transferrin precursor - rat
 N:Alternate names: lung-derived growth factor; siderophilin
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
 C:Accession: S49163; S54980; A50014; A14679; A53289; A30512; I52203

R:Becerra, H.; Pierce, A.; Codeville, B.; Gonzalez, F.; Benaisse, M.; Leger, D.; Wierus
 submitted to the EMBL Data Library, January 1994
 A:Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
 A:Reference number: S49163
 A:Accession: S49163
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <ESG>
 A:Cross-references: UNIPROT:P12346; UNIPROT:O63602; UNIPARC:UPI0000167A8E; EMBL:X77158;
 R:Becerra, H.; Pierce, A.; Codeville, B.; Gonzalez, F.; Benaisse, M.; Leger, D.; Wierus
 Biochem. J. 307, 47-55, 1995
 A:Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and g
 A:Reference number: S54980; MUID:95234054; PMID:7717992
 A:Accession: S54980
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <ESG>
 A:Cross-references: UNIPARC:UPI0000167A8E; EMBL:X77158; NID:G510195; PIDN:CAA54403.1; PI
 R:Hugenvik, J.I.; Izetda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
 Endocrinology 120, 332-340, 1987
 A:Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulati
 A:Reference number: A30014; MUID:87053639; PMID:3023031
 A:Accession: A30014
 A:Molecule type: mRNA
 A:Residues: 518-687, 'D', 689-692, 'TR', 695 <HUG>
 A:Cross-references: UNIPARC:UPI0000170B4C; GB:M27966; NID:G207439; PIDN:AAA42267.1; PID
 R:Schreiber, G.; Dryburgh, H.; Miller, A.; Matsuda, Y.; Inglis, A.; Phillips, J.; Ed
 J. Biol. Chem. 254, 12013-12019, 1979
 A:Title: The synthesis and secretion of rat transferrin.
 A:Reference number: A14679; MUID:80049855; PMID:500689
 A:Accession: A14679
 A:Molecule type: protein
 A:Residues: 20-47 <SCH>
 A:Cross-references: UNIPARC:UPI0000177C51
 R:Cavanaugh, P.G.; Nicolson, G.L.
 J. Cell. Biochem. 47, 261-271, 1991
 A:Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tum
 A:Reference number: A53289; MUID:92165927; PMID:1179188
 A:Accession: A53289
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 89, 'Y', 91, 'A', 93-99, 'W', 101-102, 'N', 233, 'AN', 236-243, 401-406, 'N', 408 <CAV>
 A:Cross-references: UNIPARC:UPI000008EF28; UNIPARC:UPI00000876D0; UNIPARC:UPI0000087E7F
 A:Experimental source: lung
 A>Note: sequence modified after extraction from NCBI backbone
 A>Note: sequence extracted from NCBI backbone (NCBI:P.86115, NCBI:P.86114)
 R:Purves, L.R.; Purves, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.
 Biochim. Biophys. Acta 966, 318-327, 1988
 A:Title: Properties of the transferrin associated with rat intestinal mucosa.
 A:Reference number: A30512; MUID:88327006; PMID:3046665
 A:Accession: A30512
 A:Molecule type: protein
 A:Residues: 20-30,639-643, 'KD', 646, 'LKACD' <PUR>
 A:Cross-references: UNIPARC:UPI0000177C52; UNIPARC:UPI0000177C53
 R:Aldred, A.R.; Howlett, G.J.; Schneider, G.
 Biochem. Biophys. Res. Commun. 122, 960-965, 1994
 A:Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bact
 A:Reference number: I52203; MUID:84307580; PMID:6236811
 A:Accession: I52203
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 7-25, 'X', 27-56, 'A', 58-64, 267-295 <RES>
 A:Cross-references: UNIPARC:UPI0000085C48; GB:M26113; NID:G207437; PIDN:AAA42266.1; PID
 C:Genetics:
 A:Gene: TF
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication
 F:20-348/Domain: transferrin repeat homology <TRH1>

Query Match 75.0%; Score 51; DB 2; Length 695;
 Best Local Similarity 69.2%; Pred. No. 1;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEEYVKAV 13
 Db 663 YEEYLGAEYVDAQ 675

RESULT 6

147228
 C:carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: 147228
 R/Roush, E.D.; Pierce, C.A.
 Biochemistry 31, 12536-12542, 1992
 A/Title: Purification and characterization of a carbonic anhydrase II inhibitor from porcine erythrocytes
 A/Reference number: 147228; PMID:9309123; EMBL:1463741
 A/Accession: 147228
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-704 <RCU>
 A/Cross-references: UNIPROT:Q29545; UNIPARC:UPI000012D142; EMBL:U36916; NID:g1016329; P1
 C/Genetic:
 A/Gene: p1CA
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication
 F/20-350/Domain: transferrin repeat homology <TRH1>

Query Match 75.0%; Score 51; DB 2; Length 704;
 Best Local Similarity 61.5%; Pred. No. 1;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEEYVKAV 13
 Db 672 YOKYLPETVDAI 684

RESULT 7

TFBOL

lactotransferrin precursor - bovine
 N/Alternate names: lactoferrin
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 09-Jul-2004
 C/Accession: 145919; S14674; S14110; S18517; J070595; S13097; S18518; S13881; P10148; S21
 R/Tsang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 PASRB 3, 6, 233, 1991
 A/Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein from bovine neutrophils
 A/Reference number: 145919
 A/Accession: 145919
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-708 <TSA>
 A/Cross-references: UNIPROT:P24627; UNIPARC:UPI0000137377; GB:L08604; NID:g163269; PIDN:
 R/Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A/Reference number: S14674
 A/Accession: S14674
 A/Molecule type: mRNA
 A/Residues: 1-144, 'V', 146-163, 'P', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <P11>
 A/Cross-references: UNIPARC:UPI000016C335; EMBL:X57084; NID:9505; PIDN:CAA0366.1; PID:9
 A/Pierce, A.; Colavizza, D.; Benalissa, M.; Maes, P.; Tartar, J.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A/Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A/Reference number: S14110; MUID:9160550; PMID:2001696
 A/Accession: S14110
 A/Molecule type: mRNA
 A/Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <P12>
 A/Cross-references: UNIPARC:UPI000017448B; EMBL:X57084
 A/Accession: S18517
 A/Molecule type: protein
 A/Residues: 20-35/82-114, 148-163, 'P', 166-178, 'V', 'P', 183-190, 205-212, 230-239, 304-339, 55
 A/Cross-references: UNIPARC:UPI000017448C; UNIPARC:UPI000017448D; UNIPARC:UPI000017448E;
 493; UNIPARC:UPI0000174494
 R/Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991

A/Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary gland
 A/Reference number: J070595; MUID:92028986; PMID:1178281
 A/Accession: J070595
 A/Molecule type: mRNA
 A/Residues: 1-65, 'PG', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A/Cross-references: UNIPARC:UPI0000174495; GB:M63502
 A/Note: the authors translated the codon CCG for residue 66 as Arg and TCT for residue 2;
 R/Mead, P.E.; Tweedie, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A/Title: cDNA and protein sequence of bovine lactoferrin.
 A/Reference number: S13097; MUID:91088328; PMID:2263492
 A/Accession: S13097
 A/Molecule type: mRNA
 A/Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A/Cross-references: UNIPARC:UPI0000174496; EMBL:X54801
 A/Accession: S18518
 A/Molecule type: protein
 A/Residues: 20-47, 59-66, 132-139, 256-277, 278, 305-333, 343-351, 361-363, 586, 587-589, 598-619
 A/Cross-references: UNIPARC:UPI0000174493; UNIPARC:UPI0000174497; UNIPARC:UPI0000174498;
 49D; UNIPARC:UPI000017449E
 R/Mead, P.E.
 submitted to the EMBL Data Library, October 1990
 A/Reference number: S13881
 A/Accession: S13881
 A/Molecule type: mRNA
 A/Residues: 28-36, 'P', 40-86, 'C', 88-708 <ME3>
 A/Cross-references: UNIPARC:UPI000017449F; EMBL:X54801
 R/Rejman, J.U.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A/Title: Purification and characterization of bovine lactoferrin from secretions of the
 49D; UNIPARC:UPI000017449E
 A/Reference number: P10148; MUID:90031466; PMID:2805645
 A/Accession: P10148
 A/Molecule type: protein
 A/Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 A/Cross-references: UNIPARC:UPI00001744A0
 R/Bellamy, W.; Takase, M.; Yamuchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A/Title: Identification of the bactericidal domain of lactoferrin.
 A/Reference number: S21756; MUID:92287941; PMID:1599934
 A/Accession: S21756
 A/Molecule type: protein
 A/Residues: 36-60 <BEL>
 A/Cross-references: UNIPARC:UPI0000475A8
 R/Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A/Title: Separation and characterization of the C-terminal half molecule of bovine lactoferrin
 A/Reference number: A56659; MUID:93253156; PMID:8486845
 A/Accession: A56659
 A/Molecule type: protein
 A/Residues: 20-25, 302-308, 359-366, 'X', 368-376, 'X', 378 <SHI>
 A/Cross-references: UNIPARC:UPI00001744A1; UNIPARC:UPI00001744A2; UNIPARC:UPI00001744A3
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-708/Product: lactotransferrin #status experimental <MAT>
 F/20-35/Domain: transferrin repeat homology <TRH1>
 F/36-60/Region: antimicrobial
 F/359-656/Domain: transferrin repeat homology <TRH2>
 F/28-64, 133-217, 176-192, 179-200, 189-202, 250-264, 367-399, 377-390, 424-703, 444-666, 476-551, 5
 F/38-55/Disulfide bonds: #status predicted
 F/79, 111, 211, 272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F/140/Binding site: carbonate (Arg) #status experimental
 F/252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/414, 452, 545, 614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F/402/Binding site: carbonate (Arg) #status experimental

QY 1 YEKYLGEEYVKAV 13
 Db 676 YEEYLGAEYVDAI 688

A:Residues: 1-711 <CHO>

A;Molecule type: protein

A:Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A:Cross-references: UNIPARC:UPI000017448A
A:Experimental source: neutrophil granulocytes
C:Genetics:
A:Gene: GDB:LTF
A:Cross-references: GDB:119368; OMIM:150210
A:Map position: 3q21-3q23
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron binding; milk
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-711/Product: lactotransferrin #status experimental <MAT>
F:21-566/Domain: transferrin repeat homology <TRH1>
F:360-699/Domain: transferrin repeat homology <TRH2>
F:39-65,39-56,135-218,177-193,190-201,251-285,503-697,595-609/Disulfide bonds: #status e
F:157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat

Query Match 70.6%; Score 48; DB 1; Length 711;
Best Local Similarity 61.5%; Pred. No. 3,4;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
DB 679 YEKYLGPQYVAGI 691

RESULT 11
S01384
transferrin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S01384; A60520; A61573
R:Balwin, G.S.; Weinstein, J.
Nucleic Acids Res. 16, 8720, 1988
A:Title: Nucleotide sequence of porcine liver transferrin.
A:Reference number: S01384; MUID:88335629; PMID:3419934
A:Accession: S01384
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-696 <BAL>
A:Cross-references: UNIPROT:P09571; UNIPARC:UPI00001130C2; EMBL:X12386; NID:g2126; PIDN:
A:Note: 308-Arg was also found
R:Balwin, G.S.; Bacic, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, E
Comp. Biochem. Physiol. B 95, 261-268, 1990
A:Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine B
A:Reference number: A60520; MUID:90227903; PMID:2328566
A:Accession: A60520
A:Molecule type: protein
A:Residues: 1-8,'X',10-11,'X',13-15 <BA2>
A:Cross-references: UNIPARC:UPI0000174485
A:Experimental source: gastric mucosa
A:Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upta
R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A:Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; MUID:91293379; PMID:2065820
A:Accession: A61573
A:Molecule type: protein
A:Residues: 1-8,'X',10-18,'XE' <CHU>
A:Cross-references: UNIPARC:UPI0000174486
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; plasma
F:1-696/Product: transferrin #status predicted <MAT>
F:1-335/Domain: transferrin repeat homology <TRH1>

Query Match 69.1%; Score 47; DB 1; Length 696;
Best Local Similarity 61.5%; Pred. No. 4,9;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
DB 655 YESYLGADYITAV 667

RESULT 12
S33761
transferrin precursor - horse
N:Alternate names: growth-promoting factor
C:Species: Equus caballus (domestic horse)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33761; S02145
R:Carpenier, M.A.; Broad, T.E.
Biochim. Biophys. Acta 1173, 230-232, 1993
A:Title: The cDNA sequence of horse transferrin.
A:Reference number: S33761; MUID:93277958; PMID:8504171
A:Accession: S33761
A:Molecule type: mRNA
A:Residues: 1-706 <CAR>
A:Cross-references: UNIPROT:P27425; UNIPARC:UPI0000137370; EMBL:M69020; NID:g164242; PIDN:
A:Experimental source: liver; developmental stage adult
R:Yoshinari, K.; Yuasa, K.; Iga, F.; Mimura, A.
Biochim. Biophys. Acta 1010, 28-34, 1989
A:Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ider
A:Reference number: S02145; MUID:89076897; PMID:2909248
A:Accession: S02145
A:Molecule type: protein
A:Residues: 20-35,'X',37,'X',39-40,'X',43-44 <YOS>
A:Cross-references: UNIPARC:UPI0000177C56
C:Complex: monomer
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-706/Product: transferrin #status experimental <MAT>
F:388-694/Domain: transferrin repeat homology <TRH2>
F:28-64,36-55,134-215,174-190,177-198,187-200,248-262,360-623,366-398,376-389,423-701,443

Query Match 66.2%; Score 45; DB 2; Length 706;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
DB 674 YKTYLGEKYITAV 686

RESULT 13
A28438
lactoferrin precursor - mouse
N:Alternate names: lactotransferrin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A28438; A41205
R:Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
A:Reference number: A92596; MUID:87280033; PMID:3611056
A:Accession: A28438
A:Molecule type: mRNA
A:Residues: 3-707 <PEN>
A:Cross-references: UNIPARC:UPI00001744A4; EMBL:J03298
R:Lin, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A:Reference number: A41205; MUID:92042099; PMID:1939212
A:Accession: A41205
A:Molecule type: DNA
A:Residues: 1-15 <LIU>
A:Cross-references: UNIPARC:UPI00001744A5; GB:M74778
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-707/Product: lactotransferrin #status predicted <MAT>
F:358-695/Domain: transferrin repeat homology <TRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.2%; Score 45; DB 1; Length 707;

Best Local Similarity 81.8%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKYLGEEYVKA 12
|||:||||
Db 676 EKYLGKEVIA 686

RESULT 14

D64326
UDPglucose 4-epimerase (EC 5.1.3.2) - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: D64326
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rsom, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:9637999; PMID:8688087
A:Accession: D64326
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-305 <BLU>
A:Cross-references: UNIPROT:Q57664; UNIPARC:UPI000012B092; GB:U67477; GB:L77117; NID:GIS
C:Genetic8:
A:Map position: FOR202715-203632
C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C:Keywords: isomerase
P:2-305/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 64.7%; Score 44; DB 2; Length 305;
Best Local Similarity 77.8%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KYLGEEYVK 11
||:||||:
Db 144 KYVGEERYK 152

RESULT 15

E75153
glyceralddehyde 3-phosphate dehydrogenase (gap) PAB0257 - Pyrococcus abyssi (strain Orsay
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E75153
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: E75153
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KAW>
A:Cross-references: UNIPROT:Q9Y1P1; UNIPARC:UPI0000034452; GB:AJ248284; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetic8:
A:Gene: gap: PAB0257
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 63.2%; Score 43; DB 2; Length 334;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEKLGEEYVKA 13
|||:||||:
Db 127 YEKALGKSYVRV 139

Search completed: June 13, 2006, 04:20:32
Job time : 15.1912 secs

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AC P02787; O43890; O9NOB8; O9UHV0;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1989, sequence version 2.
 DT 07-MAR-2006, entry version 84.
 DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal-binding globulin).
 GN Name=TF; ORFNames=PRO1400;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS TF*B2; TF*CHI AND TF*D1.
 RX MEDLINE=84194084; PubMed=6585826;
 RA Yang F., Lun J.B., McGill J.R., Moore C.M., Naylor S.L., van Bragt P.H., Baldwin W.D., Bowman B.H.;
 RT "Human transferrin: cDNA characterization and chromosomal localization."
 RT Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
 RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J., Chambon P., Cohen G.N., Zakin M.M.;
 RT "Complete structure of the human transferrin gene. Comparison with analogous chicken gene and human pseudogene."
 RT Gene 56:109-116(1987).
 RL [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=92231399; PubMed=1809186;
 RA Hershenberger C.L., Larson J.L., Arnold B., Rosteck P.R., Jr., Williams P., Depoff B., Dunn P., O'Neal K.L., Riemen M.W., Tice P.A.;
 RT "A cloned gene for human transferrin."
 RT Ann. N. Y. Acad. Sci. 646:140-154(1991).
 RL [4]
 RP NUCLEOTIDE SEQUENCE, AND VARIANT ATRANSFERRINEMIA PRO-477.
 RX MEDLINE=20563920; PubMed=11110675;
 RA Beutler E., Gelbart T., Lee F.L., Trevino R., Fernandez M.A., Fairbanks V.F.;
 RT "Molecular characterization of a case of atransferrinemia."
 RT Blood 96:4071-4074(2000).
 RL [5]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C., Ahearn M.O., Kildane S.A., Rajkumar N., Toch E.J., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>)."
 RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=22388217; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stuplenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Abramson R.D., Mullen B., Raha S.S., Lottigiano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywicki M.I., Skalek U., Smalins D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 99-698.
 RC TISSUE=fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M., He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced by analysis of cDNA clones from human fetal liver."
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RL [8]
 RP NUCLEOTIDE SEQUENCE OF 422-698.
 RX MEDLINE=84153910; PubMed=6322780;
 RA Uzan G., Fraim M., Park I., Besmond C., Maessen G., Trepat J.S., Zakin M.M., Kahn A.;
 RT "Molecular cloning and sequence analysis of cDNA for human transferrin."
 RT Biochem. Biophys. Res. Commun. 119:273-281(1984).
 RN [9]
 RP PROTEIN SEQUENCE OF 20-698.
 RX McGillivray R.T.A., Mendez E., Shevale J.G., Sinha S.K., Lineback-Zins J., Brew K.;
 RT "The primary structure of human serum transferrin. The structures of seven cyanogen bromide fragments and the assembly of the complete structure."
 RT J. Biol. Chem. 258:3543-3553(1983).
 RL [10]
 RP NUCLEOTIDE SEQUENCE OF 73-698.
 RX MEDLINE=85216459; PubMed=3858812;
 RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N., Zakin M.M.;
 RT "Organization of the human transferrin gene: direct evidence that it originated by gene duplication."
 RT Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
 RL [11]
 RP NUCLEOTIDE SEQUENCE OF 1-14.
 RX MEDLINE=87066744; PubMed=3786138;
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
 RT "The 5' region of the human transferrin gene: structure and potential regulatory sites."
 RT Nucleic Acids Res. 14:8692-8692(1986).
 RL [12]
 RP NUCLEOTIDE SEQUENCE OF 1-72 AND 291-300.
 RX MEDLINE=8712006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
 RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
 RT "The human transferrin gene: 5' region contains conserved sequences which match the control elements regulated by heavy metals, glucocorticoids and acute phase reaction."
 RT Gene 49:167-175(1986).
 RL [13]
 RP NUCLEOTIDE SEQUENCE OF 45-72.
 RX MEDLINE=20392111; PubMed=10931525;
 DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNRS>3.0.CO;2-Q;
 RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F., Espinosa de los Monteros A., de Vellos J., Zakin M.M., Baron B.;
 RT "Alternative splicing prevents transferrin secretion during differentiation of a human oligodendrocyte cell line."
 RT J. Neurosci. Res. 61:388-395(2000).
 RL [14]
 RP NUCLEOTIDE SEQUENCE OF 564-624, AND VARIANT TF*C2.
 RC TISSUE=Brain;
 RX MEDLINE=9741813; PubMed=9272172; DOI=10.1007/s004390050533;
 RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
 RT "Human transferrin (TF): a single mutation at codon 570 determines TF C1 or TF C2 variant."
 RT Hum. Genet. 100:457-458(1997).
 RL [15]
 RP NUCLEOTIDE SEQUENCE OF 564-624.
 RA Tsuchida S., Ikemoto S., Kajii E.;
 RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP NUCLEOTIDE SEQUENCE OF 636-696.

RA	Godovac-Zimmermann J.;
RT	"Isolation, characterization and N-terminal amino-acid sequence of
RL	rabbit transferrin ";
RM	Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN	[4]
RP	PROTEIN SEQUENCE OF 483-545.
RX	MEDLINE=89005676; PubMed=3169252; DOI=10.1016/0014-5793(88)80221-7;
RA	Evans R.W., Aitken A., Patel K.J.;
RT	"Evidence for a single glycan moiety in rabbit serum transferrin and
RL	location of the glycan within the polypeptide chain.";
RN	FEBS Lett. 238:39-42(1988).
RP	[5]
RX	X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC	TISSUE=Plasma;
RM	MEDLINE=89026775; PubMed=3179277;
RA	Ballley S., Evans R.W., Garratt R.C., Gorinsky B., Jhoci H., Lindley P.F.,
RT	Horsburgh C., Jhoci H., Lindley P.F., Mydin A., Sarra R., Watson J.L.;
RL	"Molecular structure of serum transferrin at 3.3-A resolution.";
RN	Biochemistry 27:5804-5812(1988).
RP	[6]
RX	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC	Sarra R., Garratt R.C., Gorinsky B., Jhoci H., Lindley P.F.;
RT	"High-resolution X-ray studies on rabbit serum transferrin:
RL	preliminary structure analysis of the N-terminal half-molecule at 2.3-
RM	A resolution.";
RA	Acta Crystallogr. B 46:763-771(1990).
RT	"- FUNCTION: Transferrins are iron binding transport proteins which
RL	can bind two Fe(3+) ions in association with the binding of an
RM	anion, usually bicarbonate. It is responsible for the transport of
RL	iron from sites of absorption and heme degradation to those of
RM	storage and utilization. Serum transferrin may also have a further
RM	role in stimulating cell proliferation.
CC	"- SUBUNIT: Monomer.
CC	"- SUBCELLULAR LOCATION: Secreted protein.
CC	"- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC	"- MISCELLANEOUS: The peptidase S60 domains do not have protease
CC	function as the catalytic residues are missing.
CC	"- SIMILARITY: Belongs to the transferrin family.
CC	"- SIMILARITY: Contains 2 peptidase S60 domains.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NonDeriv License
CC	-----
DR	EMBL; X58533; CAA41424.1; -; mRNA.
DR	EMBL; AF031625; AAB84136.1; -; Genomic DNA.
DR	EMBL; AF031611; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031612; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031613; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031614; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031615; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031616; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031617; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031618; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031619; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031620; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031621; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031622; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031623; AAB84136.1; JOINED; Genomic DNA.
DR	EMBL; AF031624; AAB84136.1; JOINED; Genomic DNA.
DR	PDB; 1JNF; X-ray; @=20-695.
DR	PDB; 1TFD; X-ray; @=20-323.
DR	MEROPS; S60_972; -.
DR	MEROPS; S60_975; -.
DR	Linkhub; P19134; -.
DR	InterPro; IPR001156; Peptidase_S60.
DR	PANTHER; PTHR11485; Peptidase_S60; 1.
DR	Pfam; PF00405; Transferrin; 2.
DR	PRINTS; P000422; TRANSFERRIN.
DR	SMART; SMO0094; TR_PER; 2.
DR	PROSITE; PS00205; TRANSFERRIN_1; 1.
DR	PROSITE; PS00206; TRANSFERRIN_2; 2.
DR	PROSITE; PS00207; TRANSFERRIN_3; 2.
KW	3D-structure; Direct protein sequencing; Glycoprotein; Ion transport;

Iron; Iron transport; Metal-binding; Methylation; Repeat; Signal;
 KM Transport. 1 19
 FT SIGNAL 20 695
 FT CHAIN 20 695
 FT DOMAIN 25 347
 FT DOMAIN 361 680
 FT METAL 82 82
 FT METAL 114 114
 FT METAL 207 268
 FT METAL 268 268
 FT METAL 411 411
 FT METAL 444 444
 FT METAL 533 533
 FT METAL 601 601
 FT BINDING 139 139
 FT BINDING 143 143
 FT BINDING 145 145
 FT BINDING 146 146
 FT BINDING 470 470
 FT BINDING 474 474
 FT BINDING 476 476
 FT BINDING 477 477
 FT MOD_RRS 42 42
 FT CARBOHYD 509 509
 FT DISULFID 28 67
 FT DISULFID 38 58
 FT DISULFID 137 213
 FT DISULFID 156 350
 FT DISULFID 177 193
 FT DISULFID 180 196
 FT DISULFID 190 198
 FT DISULFID 246 260
 FT DISULFID 358 612
 FT DISULFID 364 396
 FT DISULFID 374 387
 FT DISULFID 421 690
 FT DISULFID 436 653
 FT DISULFID 468 539
 FT DISULFID 492 681
 FT DISULFID 502 516
 FT DISULFID 513 522
 FT DISULFID 579 593
 FT DISULFID 631 636
 FT VARIANT 517 517
 FT CONFLICT 7 7
 FT CONFLICT 47 47
 FT CONFLICT 50 50
 FT STRAND 27 29
 FT STRAND 31 31
 FT HELIX 32 45
 FT TURN 46 48
 FT STRAND 49 49
 FT STRAND 51 53
 FT STRAND 59 60
 FT STRAND 62 63
 FT HELIX 72 74
 FT TURN 73 74
 FT STRAND 75 75
 FT STRAND 78 81
 FT HELIX 83 90
 FT TURN 91 94
 FT STRAND 96 102
 FT STRAND 105 105
 FT STRAND 107 109
 FT STRAND 112 112
 FT STRAND 114 121
 FT TURN 122 123
 FT TURN 128 129
 FT TURN 132 133
 FT STRAND 136 137
 FT STRAND 139 139

Serotransferrin.
 /FtId=PRO_0000035717.
 Peptidase S60 1.
 Peptidase S60 2.
 Iron 1.
 Iron 1.
 Iron 1.
 Iron 1.
 Iron 2.
 Iron 2.
 Iron 2.
 Iron 2.
 Iron 2.
 Carbonate 1.
 Carbonate 1.
 Carbonate 1; via amide nitrogen.
 Carbonate 1; via amide nitrogen.
 Carbonate 2.
 Carbonate 2.
 Carbonate 2; via amide nitrogen.
 Carbonate 2; via amide nitrogen.
 Omega-N-methylated arginine (By similarity).
 N-linked (GlcNAc. .).

V -> I.
 K -> S (in Ref. 3).
 P -> Y (in Ref. 3).

FT TURN 141 142
 FT TURN 144 147
 FT HELIX 148 154
 FT TURN 155 157
 FT STRAND 158 158
 FT STRAND 160 160
 FT STRAND 163 164
 FT HELIX 165 170
 FT TURN 171 172
 FT STRAND 173 177
 FT TURN 179 180
 FT STRAND 190 193
 FT TURN 194 195
 FT STRAND 198 200
 FT STRAND 202 206
 FT HELIX 207 214
 FT TURN 215 217
 FT STRAND 218 225
 FT TURN 226 227
 FT HELIX 228 232
 FT HELIX 236 239
 FT TURN 240 241

Query Match 85.3%; Score 58; DB 1; Length 695;
 Best Local Similarity 76.9%; Pred. No. 1.1;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEYVKAV 13
 DB 663 YEKYLGDYIKAV 675

RESULT 6
 Q6YST2_PIG PRELIMINARY; PRT; 304 AA.
 AC Q6YST2;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE Lactotransferrin (Fragment).
 GN Name=LTf;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 ON NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
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EMBL: AP006435; BAD08658.1; -; Genomic_DNA.
 HSSP: Q8TCD2; 180L.
 DR SMR: Q6YST2; 1-304.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0008199; F:ferric iron binding; IEA.
 DR GO: GO:0006879; P:iron ion homeostasis; IEA.
 DR GO: GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR01156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 1.
 DR SMART: SM00422; TRANSFERRIN.
 DR PRINTS: SM00094; TR_FER_1.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00206; TRANSFERRIN_2; 1.
 DR PROSITE: PS00207; TRANSFERRIN_3; 1.
 FT NON TER 1 1
 SO SEQUENCE 304 AA; 3315 MW; 16C0B1675D8722A8 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 304;

Best Local Similarity 76.9%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
Db 272 YEKYLGEYVAV 284

RESULT 7
Q7TSX8_MARMO PRELIMINARY; PRT; 694 AA.
AC Q7TSX8;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Sciuridae; Xerinae; Marmotini; Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Rinaudo J.A.S., Gerin J.L.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL -----
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CC -----
DR EMBL; AY288100; AAP37129.1; -; mRNA.
DR HSSP; P19134; 1JNF.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:feric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 694 AA; 76466 MW; 4005F7D1CFC8A7 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 694;
Best Local Similarity 84.6%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
Db 662 YEKYLGEYVAV 674

RESULT 8
TRFL_PIG STANDARD; PRT; 704 AA.
ID TRFL_PIG
AC P14632; Q29557;
DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
DT 15-DEC-1998, sequence version 3.
DT 07-FEB-2006, entry version 46.
DE Lactotransferrin precursor (EC 3.4.21.-) (Lactoferrin).
GN Name=LTR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=92379101; PubMed=1511016; DOI=10.1016/0167-4781(92)90061-4;
RA Lyndon J.P., O'Malley B.R., Saucedo O., Lee T., Heaton D.R.,

RA Connely O.M.;
RT "Nucleotide and primary amino acid sequence of porcine lactoferrin.";
RL Biochim. Biophys. Acta 1132:97-99 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=92367939; PubMed=1503259;
RA Alexander L.J., Levine W.B., Teng C.T., Beattie C.W.;
RT "Cloning and sequencing of the porcine lactoferrin cDNA.";
RL Anim. Genet. 23:251-256 (1992).
RN [3]
RP PROTEIN SEQUENCE OF 20-49.
RX MEDLINE=90105538; PubMed=2605266;
RA Hutcheson T.W., Magnuson J.S., Yip T.-T.;
RT "Rapid purification of porcine colostrum whey lactoferrin by affinity
RT chromatography on single-stranded DNA-agarose. Characterization, amino
RT acid composition and N-terminal amino acid sequence.";
RL Biochim. Biophys. Acta 999:323-329 (1989).
CC - FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two Fe(3+) ions in association with the binding of an
CC anion, usually bicarbonate.
CC - FUNCTION: The lactotransferrin peptidase S60 domain 1 functions as
CC a serine protease that cuts arginine rich regions. This function
CC contributes to the antimicrobial activity (By similarity).
CC - CATALYTIC ACTIVITY: Preferential at -Arg-Ser-Arg-|- and -Arg-
CC Arg-Ser-Arg-|- and of Z-Phe-Arg-|-aminomethylcoumarin.
CC - SUBUNIT: Monomer.
CC - SUBCELLULAR LOCATION: Secreted protein.
CC - MISCELLANEOUS: The second peptidase S60 domain does not have
CC protease function as the catalytic residues are missing.
CC - SIMILARITY: Belongs to the transferrin family.
CC - SIMILARITY: Contains 2 peptidase S60 domains.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; M92089; AAA31102.1; -; mRNA.
DR EMBL; M81327; AAA31059.1; -; mRNA.
DR PIR; A45543; A45543.
DR HSSP; Q9TUM0; 1DTZ.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Ion transport;
KW Iron; Iron transport; Metal-binding; Protease; Repeat;
KW Serine protease; Signal; Transport.
FT SIGNAL 1 19
FT CHAIN 20 704
FT DOMAIN 25 348
FT DOMAIN 360 689
FT ACT_SITE 88 88
FT ACT_SITE 274 274
FT METAL 77 77
FT METAL 107 107
FT METAL 207 207
FT METAL 268 268
FT METAL 410 410
FT METAL 448 448
FT METAL 541 541
FT METAL 610 610
FT BINDING 132 132
FT BINDING 136 136
FT BINDING 138 138
FT BINDING 139 139
FT BINDING 474 474
FT BINDING 478 478

Lactotransferrin.
/FTID=PRO_0000035728.
Peptidase S60 1.
Peptidase S60 2.
Catalytic dyad (By similarity).
Catalytic dyad (By similarity).
Iron 1 (By similarity).
Iron 1 (By similarity).
Iron 1 (By similarity).
Iron 2 (By similarity).
Iron 2 (By similarity).
Iron 2 (By similarity).
Iron 2 (By similarity).
Iron 2 (By similarity).
Iron 2 (By similarity).
Carbonate 1 (By similarity).
Carbonate 1 (By similarity).
Carbonate 1; via amide nitrogen (By similarity).
Carbonate 1; via amide nitrogen (By similarity).
Carbonate 2 (By similarity).
Carbonate 2 (By similarity).

```
FT BINDING 480 480 Carbonate 2; via amide nitrogen (By  
FT BINDING 481 481 similarity).  
FT CARBOHYD 385 385 Carbonate 2; via amide nitrogen (By  
FT CARBOHYD 491 491 similarity).  
FT DISULFID 28 62 N-linked (GLCNAC. . .) (Potential).  
FT DISULFID 38 53 By similarity.  
FT DISULFID 130 213 By similarity.  
FT DISULFID 172 188 By similarity.  
FT DISULFID 185 196 By similarity.  
FT DISULFID 246 260 By similarity.  
FT DISULFID 363 395 By similarity.  
FT DISULFID 373 386 By similarity.  
FT DISULFID 420 699 By similarity.  
FT DISULFID 472 547 By similarity.  
FT DISULFID 496 690 By similarity.  
FT DISULFID 506 520 By similarity.  
FT DISULFID 517 530 By similarity.  
FT DISULFID 588 602 By similarity.  
FT DISULFID 640 645 By similarity.  
FT CONFLICT 12 12 G -> W (in Ref. 1).  
FT CONFLICT 46 48 RRT -> TTR (in Ref. 3).  
FT CONFLICT 51 51 M -> I (in Ref. 1).  
FT CONFLICT 85 85 D -> G (in Ref. 2).  
FT CONFLICT 121 121 Missing (in Ref. 2).  
FT CONFLICT 132 132 T -> I (in Ref. 1).  
FT CONFLICT 284 284 E -> S (in Ref. 1).  
FT CONFLICT 573 573 E -> Q (in Ref. 1).  
FT CONFLICT 590 590 D -> N (in Ref. 1).  
FT CONFLICT 625 625 V -> M (in Ref. 1).  
FT CONFLICT 662 662 V -> C (in Ref. 1).  
FT CONFLICT 686 704 NLKQSVPLLEACAFMR -> T (in Ref. 1).  
SQ SEQUENCE 704 AA; 77626 MM; 93261EFD608AD358 CRC64;
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Query Match 82.4%; Score 56; DB 1; Length 704;  
Best Local Similarity 76.9%; Pred. No. 2.3;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 YEKYLGESEYVAV 13  
Db 672 YEKYLGESEYVAVI 684
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RESULT 9  
ID 06YT39_PIG PRELIMINARY; PRT; 704 AA.  
AC 06YT39;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, sequence version 1.  
DE Lactoferrin.  
GN Name:LF;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;  
OC Sus.  
OX NCBI_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.,  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
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EMBL, AP006185; BAD08651.1; -; Genomic_DNA.  
DR HSSP; Q29477; IUM1.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008199; F:ferriic iron binding; IEA.  
DR GO; GO:0006879; P:iron ion homeostasis; IEA.  
DR GO; GO:0006826; P:iron ion transport; IEA.  
DR InterPro; IPR001156; Peptidase_S60.
```

```
DR PANTHER; PTHR11485; Peptidase_S60; 1.  
DR Pfam; PF00405; Transferin; 2.  
DR PRINTS; PR00422; TRANSFERRIN.  
DR SMART; SM00094; TR_FER; 2.  
DR PROSITE; PS00205; TRANSFERRIN_1; 2.  
DR PROSITE; PS00206; TRANSFERRIN_2; 2.  
DR PROSITE; PS00207; TRANSFERRIN_3; 1.  
SQ SEQUENCE 704 AA; 77612 MM; 10DFEA3C136ED5DA CRC64;
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Query Match 82.4%; Score 56; DB 2; Length 704;  
Best Local Similarity 76.9%; Pred. No. 2.3;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 YEKYLGESEYVAV 13  
Db 672 YEKYLGESEYVAVI 684
```

```
RESULT 10  
ID 07YS20_PIG PRELIMINARY; PRT; 704 AA.  
AC 07YS20;  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE Lactoferrin.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;  
OC Sus.  
OX NCBI_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Tissue=Mammary gland;  
RA Pecorini C., Fogher C., Baldi A.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
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EMBL, AY306198; AAP70487.1; -; mRNA.  
DR HSSP; P24627; INKX.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008199; F:ferriic iron binding; IEA.  
DR GO; GO:0006879; P:iron ion homeostasis; IEA.  
DR GO; GO:0006826; P:iron ion transport; IEA.  
DR InterPro; IPR001156; Peptidase_S60.  
DR PANTHER; PTHR11485; Peptidase_S60; 1.  
DR Pfam; PF00405; Transferin; 2.  
DR PRINTS; PR00422; TRANSFERRIN.  
DR SMART; SM00094; TR_FER; 2.  
DR PROSITE; PS00205; TRANSFERRIN_1; 2.  
DR PROSITE; PS00206; TRANSFERRIN_2; 1.  
DR PROSITE; PS00207; TRANSFERRIN_3; 1.  
SQ SEQUENCE 704 AA; 77523 MM; AAC8B1767E56BF6A CRC64;  
Query Match 82.4%; Score 56; DB 2; Length 704;  
Best Local Similarity 76.9%; Pred. No. 2.3;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 YEKYLGESEYVAV 13  
Db 672 YEKYLGESEYVAVI 684  
RESULT 11  
ID 08WMN8_PIG PRELIMINARY; PRT; 704 AA.  
AC 08WMN8;  
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2002, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE Lactoferrin (Fragment).
```

```

GN Name=LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Wang S.-R., Lin T.-Y., Meng C.-N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; L77887; AAL40161.1; -, mRNA.
DR HSSP; P24627; INKX.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:feric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
DR NON_TER 1
SQ SEQUENCE 704 AA; 77682 MW; 64EE769F7503CC32 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.3;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
Db 672 YEKYLGEYKAV 684

RESULT 12
TRFL CAPHI STANDARD; PRT; 708 AA.
AC Q29477; Q29479;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 41.
DE Lactoferrin precursor (EC 3.4.21.-) (Lactoferrin).
GN Name=LTF;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Mammary gland;
RA Lee T., Yu S., Kim S., Lee K., Yu D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=9438047; PubMed=8093048;
RA le Provost F., Nocart M., Guerin G., Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U2 synteny group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two Fe(3+) ions in association with the binding of an
CC anion, usually bicarbonate.
CC -1- FUNCTION: The lactotransferrin peptidase S60 domain 1 functions as
CC a serine protease that cuts arginine rich regions. This function

```

```

CC contributes to the antimicrobial activity (By similarity).
CC -1- CATALYTIC ACTIVITY: Preferential at -Arg-Ser-Arg-|- and -Arg-
CC Arg-Ser-Arg-|- and of 2-Phe-Arg-|- aminomethylcoumarin.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- MISCELLANEOUS: The second peptidase S60 domain does not have
CC protease function as the catalytic residues are missing.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -1- SIMILARITY: Contains 2 peptidase S60 domains.
-----
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DR EMBL; U53857; AA97958.1; -, mRNA.
DR EMBL; X78902; CA55517.1; -, mRNA.
DR PDB; 1JW1; X-ray; A=20-708.
DR MEROPS; S60.001; -.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Glycoprotein; Hydrolase; Ion transport; Iron;
KW Iron transport; Metal-binding; Protease; Repeat; Serine protease;
KW Signal; Transport.
FT SIGNAL 1
FT CHAIN 20
FT DOMAIN 25
FT ACT_SITE 92
FT ACT_SITE 278
FT METAL 79
FT METAL 111
FT METAL 211
FT METAL 272
FT METAL 414
FT METAL 414
FT METAL 452
FT METAL 452
FT METAL 545
FT METAL 614
FT BINDING 140
FT BINDING 142
FT BINDING 143
FT BINDING 143
FT BINDING 478
FT BINDING 482
FT BINDING 484
FT BINDING 485
FT CARBOHYD 252
FT CARBOHYD 300
FT CARBOHYD 387
FT CARBOHYD 495
FT CARBOHYD 495
FT CARBOHYD 564
FT DISULFID 38
FT DISULFID 64
FT DISULFID 134
FT DISULFID 176
FT DISULFID 189
FT DISULFID 200
FT DISULFID 260
FT DISULFID 367
FT DISULFID 377
FT DISULFID 390
FT DISULFID 424
FT DISULFID 444
FT DISULFID 476
FT DISULFID 500
FT DISULFID 524
FT DISULFID 534

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FT DISULFID 592 606 By similarity.
FT DISULFID 644 649 I -> V (in Ref. 2).
FT CONFLICT 56 56 L -> R (in Ref. 2).
FT CONFLICT 88 88 Q -> K (in Ref. 2).
FT CONFLICT 124 124 F -> P (in Ref. 2).
FT CONFLICT 154 154 S -> R (in Ref. 2).
FT CONFLICT 304 304 D -> G (in Ref. 2).
FT CONFLICT 414 414
FT TURN 21 22
FT STRAND 23 24
FT STRAND 26 32
FT TURN 33 35
FT STRAND 36 37
FT HELIX 38 48
FT STRAND 49 51
FT STRAND 54 57
FT TURN 60 60
FT STRAND 61 65
FT TURN 66 69
FT HELIX 70 71
FT TURN 72 73
FT STRAND 77 78
FT STRAND 80 80
FT TURN 81 87
FT STRAND 88 91
FT STRAND 93 95
FT STRAND 99 103
FT TURN 104 105
FT STRAND 106 111
FT TURN 119 120
FT HELIX 125 127
FT STRAND 129 132
FT STRAND 135 136
FT STRAND 138 139
FT HELIX 141 145
FT STRAND 146 146
FT TURN 147 148
FT STRAND 149 151
FT HELIX 153 155
FT TURN 159 161
FT STRAND 162 162
FT TURN 164 166
FT STRAND 167 174
FT STRAND 178 180
FT TURN 182 184
FT STRAND 186 186
FT TURN 187 188
FT STRAND 189 191
FT STRAND 194 194
FT TURN 196 197
FT STRAND 198 198
FT TURN 199 200
FT STRAND 202 203
FT TURN 204 205
FT STRAND 206 210
FT TURN 211 213
FT STRAND 214 215
FT HELIX 216 219
FT STRAND 220 223
FT STRAND 225 225
FT STRAND 227 227
FT STRAND 230 232
FT HELIX 233 236
FT STRAND 240 240
FT TURN 241 242
FT STRAND 243 245
FT TURN 251 252
FT STRAND 253 253
FT TURN 258 259
FT TURN 261 264
FT STRAND 266 266
FT STRAND 269 270
FT STRAND 273 281

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FT HELIX 283 286
FT TURN 287 287
FT HELIX 288 291
FT TURN 292 297
FT TURN 299 300
FT STRAND 301 302
FT STRAND 304 305
FT TURN 307 308
FT TURN 312 313
FT STRAND 318 319
FT TURN 321 322
FT STRAND 325 326
FT TURN 331 332
FT HELIX 335 338
FT STRAND 339 339
FT STRAND 341 343
FT TURN 344 348
FT HELIX 349 351
FT STRAND 352 352
FT STRAND 354 358
FT TURN 359 361
FT STRAND 362 362
FT STRAND 364 366
FT STRAND 370 372

Query Match 80.9%; Score 55; DB 1; Length 708;
Best Local Similarity 76.9%; Pred. No. 3.4;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YEKYLGEYVYKAV 13
Db 676 YEKYLGEYVYAI 688

RESULT 13
OSMJB8 SHEEP PRELIMINARY; PRT; 708 AA.
ID OSMJB8;
AC OSMJB8;
DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Lactoferrin.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Grover S., Geetha N., Mohanty A.K., Kitamura Y., Batish V.K.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL: AY792499; AAY92908.1; -; mRNA.
CC SMR: OSMJB8; 22-708.
DR GO: GO:000576; C:extracellular region; IEA.
DR GO: GO:0008199; P:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001156; Peptidase_S60.
DR PANTHER: PTHR11485; Peptidase_S60; 1.
DR Pfam: PF00405; Transferrin; 2.
DR PRINTS: PRO0422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 708 AA; 77236 MW; BOAEFEFC9BBA2CC CRC64;

Query Match 80.9%; Score 55; DB 2; Length 708;

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Best Local Similarity 76.9%; Pred. No. 3.4;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVYKAV 13
Db 676 YEKYLGEYVYTAI 688

RESULT 14

O8MI10_BOVIN PRELIMINARY; PRT; 355 AA.
AC O8MI10;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Lactotransferrin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=91160550; PubMed=2001696;
RA Pierce A., Colavizza D., Benaisse M., Maes P., Tartar A.,
RA Montreuil J., Spik G.;
RL Eur. J. Biochem. 196;177-184(1991).
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DR EMBL: X17066; CA34912.1; -, mRNA.
DR HSSP: P24627; 1BLF.
DR SMR; O8MI10; 8-347.
DR Ensemble1; ENSBTAG0000001292; Bos taurus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
FT NON TER 1
SQ SEQUENCE 355 AA; 38861 MW; 92CF0C274BEC6893 CRC64;
Query Match 75.0%; Score 51; DB 2; Length 355;
Best Local Similarity 69.2%; Pred. No. 8;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary;
RX MEDLINE=9108328; PubMed=2261492;
RA Mead P.E., Tweedie J.W.;
RT "cDNA and protein sequence of bovine lactoferrin.";
RL Nucleic Acids Res. 18:7167-7167(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary;
RA Tweedie J.;
RL Submitted (JAN-1991) to the EMBL/GenBank/DBJ databases.
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DR EMBL: X54801; CA38572.1; -, mRNA.
DR HSSP; Q29477; 1JW1.
DR SMR; O6LBN7; 1-681.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PANTHER; PTHR11485; Peptidase_S60; 1.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
FT CHAIN <1 681 Bovine Lactoferrin.
FT NON TER 1
SQ SEQUENCE 681 AA; 75182 MW; 4927DE88144D99BA CRC64;

Query Match 75.0%; Score 51; DB 2; Length 681;
Best Local Similarity 69.2%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVYKAV 13
Db 649 YEKYLGEYVYTAI 661

Search completed: June 13, 2006, 04:17:46
Job time : 105.956 secs

RESULT 15
O6LBN7_BOVIN PRELIMINARY; PRT; 681 AA.
AC O6LBN7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Lactoferrin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:20:54 ; Search time 22.9412 Seconds
(without alignments)
49.601 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEERYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /EMC_Ceiera_SIDS3/prodata/2/iaa/5.COMB.pep.*
 - 2: /EMC_Ceiera_SIDS3/prodata/2/iaa/6.COMB.pep.*
 - 3: /EMC_Ceiera_SIDS3/prodata/2/iaa/7.COMB.pep.*
 - 4: /EMC_Ceiera_SIDS3/prodata/2/iaa/H.COMB.pep.*
 - 5: /EMC_Ceiera_SIDS3/prodata/2/iaa/PCTUS.COMB.pep.*
 - 6: /EMC_Ceiera_SIDS3/prodata/2/iaa/RE.COMB.pep.*
 - 7: /EMC_Ceiera_SIDS3/prodata/2/iaa/bcckfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	696	7 US-08-175-158A-2	Patent No. 5262177
2	68	100.0	698	1 US-09-439-740-2	Sequence 2, Appli
3	68	100.0	698	2 US-08-470-058-2	Sequence 2, Appli
4	68	100.0	1074	1 US-09-037-188-2	Sequence 2, Appli
5	68	100.0	1074	2 US-09-265-310-2	Sequence 2, Appli
6	68	100.0	1074	2 US-09-753-385-2	Sequence 2, Appli
7	68	100.0	1410	1 US-08-470-058-4	Sequence 4, Appli
8	68	100.0	1410	2 US-09-037-188-4	Sequence 4, Appli
9	68	100.0	1410	2 US-09-265-310-4	Sequence 4, Appli
10	68	100.0	1410	2 US-09-753-385-4	Sequence 4, Appli
11	68	100.0	703	1 US-08-453-703-6	Sequence 6, Appli
12	56	82.4	703	1 US-08-456-106-6	Sequence 6, Appli
13	56	82.4	703	1 US-08-456-108-6	Sequence 6, Appli
14	56	82.4	703	1 US-09-265-577-6	Sequence 6, Appli
15	56	82.4	703	2 US-09-633-739-6	Sequence 6, Appli
16	56	82.4	708	1 US-08-145-681-4	Sequence 4, Appli
17	56	82.4	708	1 US-08-453-703-4	Sequence 4, Appli
18	51	75.0	708	1 US-08-456-106-4	Sequence 4, Appli
19	51	75.0	708	2 US-08-456-108-4	Sequence 4, Appli
20	51	75.0	708	2 US-09-265-577-4	Sequence 4, Appli
21	51	75.0	708	2 US-09-633-739-4	Sequence 4, Appli
22	51	75.0	690	2 US-10-077-381-4	Sequence 2, Appli
23	48	70.6	694	2 US-08-476-798-2	Sequence 2, Appli
24	48	70.6	711	2 US-09-265-577-2	Sequence 2, Appli
25	48	70.6	711	2 US-08-461-313-2	Sequence 2, Appli
26	48	70.6	694	2 US-09-421-632-2	Sequence 2, Appli

ALIGNMENTS

27	48	70.6	694	2 US-09-932-190-2	Sequence 2, Appli
28	48	70.6	705	1 US-08-655-640-2	Sequence 2, Appli
29	48	70.6	708	1 US-08-655-640-4	Sequence 4, Appli
30	48	70.6	709	1 US-08-154-019-2	Sequence 2, Appli
31	48	70.6	709	2 US-08-461-313-2	Sequence 2, Appli
32	48	70.6	709	2 US-08-464-167-2	Sequence 2, Appli
33	48	70.6	709	2 US-09-158-313-2	Sequence 2, Appli
34	48	70.6	709	2 US-08-476-798-2	Sequence 2, Appli
35	48	70.6	711	1 US-08-145-681-2	Sequence 2, Appli
36	48	70.6	711	1 US-08-250-308-2	Sequence 2, Appli
37	48	70.6	711	1 US-08-154-019-4	Sequence 4, Appli
38	48	70.6	711	1 US-08-461-313-4	Sequence 4, Appli
39	48	70.6	711	1 US-08-453-703-2	Sequence 2, Appli
40	48	70.6	711	1 US-08-456-106-2	Sequence 2, Appli
41	48	70.6	711	1 US-08-464-167-4	Sequence 2, Appli
42	48	70.6	711	2 US-09-158-313-4	Sequence 4, Appli
43	48	70.6	711	2 US-08-456-108-2	Sequence 2, Appli
44	48	70.6	711	2 US-08-476-798-4	Sequence 2, Appli
45	48	70.6	711	2 US-09-265-577-2	Sequence 2, Appli

RESULT 1
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. OSEPH P.; ESTIN, CHARLES D.; FLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGERD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUWAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO: 4:
LENGTH: 696
5262177-4

Query Match 100.0%; Score 68; DB 7; Length 696;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
Db 664 YEKYLGEERYKAV 676

RESULT 2
US-08-175-158A-2
Sequence 2, Application US/08/75158A
Patent No. 5986067
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MACGILLIVRAY, Ross T. A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODMORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
NUMBER OF SEQUENCES: 7
NUMBER OF INVENTION: MOLECULES AND MUTANTS THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,158A
FILING DATE: 28-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,029
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-175-158A-2

Query Match      100.0%; Score 68; DB 1; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      666 YEKYLGEYVKAV 678

RESULT 3
US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MAGGILLIVRAY, Ross T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match      100.0%; Score 68; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      666 YEKYLGEYVKAV 678

RESULT 4
US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
NUMBER OF SEQUENCES: 12
TITLE OF INVENTION: of a Selected Substance Into Cells
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TK193-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match      100.0%; Score 68; DB 1; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      1042 YEKYLGEYVKAV 1054

RESULT 5
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
```

APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 100.0%; Score 68; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
DB 1042 YEKYLGEYVAV 1054

RESULT 6
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 100.0%; Score 68; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
DB 1042 YEKYLGEYVAV 1054

RESULT 7
US-09-753-385-2
Sequence 2, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
TITLE OF INVENTION: OF A SELECTED SUBSTANCE INTO CELLS
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1074
TYPE: PRT
ORGANISM: Homo sapiens
US-09-753-385-2

Query Match 100.0%; Score 68; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
DB 1042 YEKYLGEYVAV 1054

RESULT 8
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.

TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TK793-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 100.0%; Score 68; DB 1; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
Db 1378 YEKYLGEYKAV 1390

RESULT 9
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 100.0%; Score 68; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
Db 1378 YEKYLGEYKAV 1390

RESULT 10
US-09-285-310-4
Sequence 4, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 100.0%; Score 68; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YKYLGEYVAV 13
Db 1378 YKYLGEYVAV 1390

RESULT 11
US-09-753-385-4
Sequence 4, Application US/09753385
Patent No. 6858578
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
FILE REFERENCE: 10278-025004
CURRENT APPLICATION NUMBER: US/09/753,385
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 08/470,058
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 09/037,188
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 09/285,310
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1410
TYPE: PRT
ORGANISM: Homo sapiens
US-09-753-385-4

Query Match 100.0%; Score 68; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YKYLGEYVAV 13
Db 1378 YKYLGEYVAV 1390

RESULT 12
US-08-145-681-6
Sequence 6, Application US/08145681
Patent No. 5571691
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Bots, L.L.P.
STREET: 910 Louisiana St
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGregor, Martin L.

REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 19928-0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/229/1874
TELEFAX: 713/229/1522
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-145-681-6

Query Match 82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YKYLGEYVAV 13
Db 671 YKYLGEYVAV 683

RESULT 13
US-08-453-703-6
Sequence 6, Application US/08453703
Patent No. 5766939
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO

ORIGINAL SOURCE:
US-08-453-703-6
ORGANISM: Sus scrofa

Query Match 82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVYKAV 13
Db 671 YEKYLGEYVYTAI 683

RESULT 14
US-08-456-106-6
Sequence 6, Application US/08456106
Patent No. 5849881
GENERAL INFORMATION:
APPLICANT: Connely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/456,106
APPLICATION NUMBER: 435
CLASSIFICATION: 435
FILING DATE: Concurrently herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3660
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-106-6

Query Match 82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVYKAV 13
Db 671 YEKYLGEYVYTAI 683

RESULT 15
US-08-456-108-6
Sequence 6, Application US/08456108
Patent No. 6100054
GENERAL INFORMATION:
APPLICANT: Connely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/456,108
APPLICATION NUMBER: 435
CLASSIFICATION: 435
FILING DATE: Concurrently herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-023
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3660
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-108-6

Query Match 82.4%; Score 56; DB 2; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVYKAV 13
Db 671 YEKYLGEYVYTAI 683

Search completed: June 13, 2006, 04:25:48
Job time : 22.9412 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:24 ; Search time 74.75 Seconds
(without alignments)
80.559 Million cell updates/sec

Title: US-10-612-162a-4
Perfect score: 68
Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-612-162-4	Sequence 4, Appli
2	68	100.0	49	US-10-378-094-16	Sequence 16, Appli
3	68	100.0	49	US-10-384-060-38	Sequence 38, Appli
4	68	100.0	49	US-10-231-494-27	Sequence 27, Appli
5	68	100.0	137	US-10-383-201-12	Sequence 12, Appli
6	68	100.0	328	US-09-891-126-5	Sequence 5, Appli
7	68	100.0	328	US-10-266-745-5	Sequence 5, Appli
8	68	100.0	679	US-10-378-094-3	Sequence 3, Appli
9	68	100.0	679	US-10-384-060-3	Sequence 3, Appli
10	68	100.0	679	US-10-231-494-3	Sequence 3, Appli
11	68	100.0	679	US-10-429-482-4	Sequence 4, Appli
12	68	100.0	679	US-10-429-497-4	Sequence 4, Appli
13	68	100.0	679	US-10-429-515-4	Sequence 4, Appli
14	68	100.0	679	US-10-428-598-4	Sequence 4, Appli
15	68	100.0	679	US-10-428-635-4	Sequence 4, Appli
16	68	100.0	679	US-10-428-653-4	Sequence 4, Appli
17	68	100.0	679	US-10-429-659-4	Sequence 4, Appli
18	68	100.0	679	US-10-429-661-4	Sequence 4, Appli
19	68	100.0	679	US-10-429-664-4	Sequence 4, Appli
20	68	100.0	679	US-10-428-662-4	Sequence 4, Appli
21	68	100.0	679	US-10-428-655-4	Sequence 4, Appli
22	68	100.0	679	US-10-429-654-4	Sequence 4, Appli
23	68	100.0	698	US-09-935-642-6	Sequence 6, Appli
24	68	100.0	698	US-10-378-094-2	Sequence 2, Appli
25	68	100.0	698	US-10-384-060-2	Sequence 2, Appli
26	68	100.0	698	US-10-231-494-2	Sequence 2, Appli
27	68	100.0	698	US-10-383-201-10	Sequence 10, Appli

28	68	100.0	698	US-10-383-201-14	Sequence 14, Appli
29	68	100.0	698	US-10-887-711-2	Sequence 2, Appli
30	68	100.0	698	US-10-513-523-3	Sequence 3, Appli
31	68	100.0	698	US-11-177-506-46	Sequence 46, Appli
32	68	100.0	698	US-11-038-901-2	Sequence 2, Appli
33	68	100.0	1074	US-09-753-385-2	Sequence 2, Appli
34	68	100.0	1410	US-09-753-385-4	Sequence 4, Appli
35	68	100.0	1410	US-10-473-127-805	Sequence 805, App
36	68	100.0	1418	US-10-473-127-804	Sequence 804, App
37	56	82.4	15	US-10-769-514-14	Sequence 14, Appli
38	56	82.4	15	US-10-769-514-47	Sequence 47, Appli
39	56	82.4	703	US-10-620-256-6	Sequence 273, App
40	51	75.0	695	US-10-316-253-273	Sequence 273, App
41	51	75.0	698	US-10-316-253-275	Sequence 275, App
42	51	75.0	698	US-10-205-331-55	Sequence 55, Appli
43	51	75.0	708	US-10-169-297-8	Sequence 8, Appli
44	51	75.0	708	US-10-620-256-4	Sequence 4, Appli
45	51	75.0	708	US-10-513-523-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-10-612-162-4
; Sequence 4, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; TITLE OF INVENTION: antibodies, their preparation and use
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612.162
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-612-162-4

Query Match      100.0%; Score 68; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      1 YEKYLGEYVKAV 13

RESULT 2
US-10-378-094-16
; Sequence 16, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378.094
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231.494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745

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;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 16
;; LENGTH: 49
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: C2 subdomain of transferrin
US-10-378-094-16

Query Match 100.0%; Score 68; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
Db 37 YEKYLGEYVKAV 49

RESULT 3
US-10-384-060-38
; Sequence 38, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: C2 domain of huma Tf
US-10-384-060-38

Query Match 100.0%; Score 68; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
Db 37 YEKYLGEYVKAV 49

RESULT 4
US-10-231-494-27
; Sequence 27, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059

;; PRIOR FILING DATE: 2001-11-30
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 27
;; LENGTH: 49
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Transferrin
US-10-231-494-27

Query Match 100.0%; Score 68; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
Db 37 YEKYLGEYVKAV 49

RESULT 5
US-10-383-201-12
; Sequence 12, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; PRIOR FILING DATE: 2003-03-06
; CURRENT APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-12

Query Match 100.0%; Score 68; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
Db 105 YEKYLGEYVKAV 117

RESULT 6
US-09-891-126-5
; Sequence 5, Application US/09891126
; Patent No. US20020072596A1
; GENERAL INFORMATION:


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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035P1
; CURRENT APPLICATION NUMBER: US/09/891,126
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-126-5

Query Match          100.0%; Score 68; DB 3; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYKAV 13
        |||||
Db       296 YEKYLGEYKAV 308

RESULT 7
US-10-266-745-5
; Sequence 5, Application US/10266745
; Publication No. US20030149256A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035P1
; CURRENT APPLICATION NUMBER: US/10/266,745
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-745-5

Query Match          100.0%; Score 68; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYKAV 13
        |||||
Db       296 YEKYLGEYKAV 308

RESULT 8
US-10-378-094-3
; Sequence 3, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
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; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3

Query Match          100.0%; Score 68; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYKAV 13
        |||||
Db       647 YEKYLGEYKAV 659

RESULT 9
US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match          100.0%; Score 68; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYKAV 13
        |||||
Db       647 YEKYLGEYKAV 659

RESULT 10
US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
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; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3
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Query Match          100.0%; Score 68; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 YEKYLGEYVKAV 13
Db      647 YEKYLGEYVKAV 659
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RESULT 11
US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tu
; FILE REFERENCE: 2537.000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-482-4
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Query Match          100.0%; Score 68; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 YEKYLGEYVKAV 13
Db      647 YEKYLGEYVKAV 659
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RESULT 12
US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment of Tumors
; FILE REFERENCE: 2537.000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4
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Query Match          100.0%; Score 68; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 YEKYLGEYVKAV 13
Db      647 YEKYLGEYVKAV 659
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RESULT 13
US-10-429-515-4
; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537.000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4
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Query Match          100.0%; Score 68; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 YEKYLGEYVKAV 13
Db      647 YEKYLGEYVKAV 659
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RESULT 14
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment of Tumors
; FILE REFERENCE: 2537.000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4
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Query Match          100.0%; Score 68; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 YEKYLGEYVKAV 13
Db      647 YEKYLGEYVKAV 659
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RESULT 15
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537.000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
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; LENGTH: 679
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-429-635-4

Query Match 100.0%; Score 68; DB 5; Length 679;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEEYKAV 13
 |||||
 Db 647 YEKYLGEEYKAV 659

Search completed: June 13, 2006, 04:56:23
 Job time : 75.75 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 04:49:58 ; Search time 4.39706 Seconds
(without alignments)
37.380 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues
Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB pep: *
3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB pep: *
4: /EMC_Celerra_SIDS3/prodata/1/pubppa/US08_NEW_PUB pep: *
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6: /EMC_Celerra_SIDS3/prodata/1/pubppa/US10_NEW_PUB pep: *
7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB pep: *
8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	49	6	US-10-515-429-27 Sequence 27, Appl
2	68	100.0	679	6	US-10-515-429-3 Sequence 3, Appl
3	68	100.0	698	6	US-10-515-429-2 Sequence 2, Appl
4	58	85.3	676	6	US-10-515-429-37 Sequence 37, Appl
5	56	82.4	686	7	US-11-258-767-36 Sequence 37, Appl
6	56	82.4	703	7	US-11-258-767-37 Sequence 37, Appl
7	55	80.9	708	7	US-11-258-767-28 Sequence 28, Appl
8	55	80.9	708	7	US-11-258-767-32 Sequence 32, Appl
9	51	75.0	676	6	US-10-515-429-38 Sequence 38, Appl
10	51	75.0	681	7	US-11-258-767-13 Sequence 13, Appl
11	51	75.0	698	7	US-11-258-767-25 Sequence 25, Appl
12	51	75.0	708	7	US-11-258-767-16 Sequence 16, Appl
13	51	75.0	708	7	US-11-258-767-19 Sequence 19, Appl
14	51	75.0	708	7	US-11-258-767-22 Sequence 22, Appl
15	51	75.0	708	7	US-11-258-767-29 Sequence 29, Appl
16	51	75.0	708	7	US-11-258-767-35 Sequence 35, Appl
17	51	75.0	708	7	US-11-258-767-38 Sequence 38, Appl
18	51	75.0	708	7	US-11-258-767-39 Sequence 39, Appl
19	49	72.1	695	7	US-11-258-767-36 Sequence 26, Appl
20	48	70.6	685	6	US-10-515-429-41 Sequence 41, Appl
21	48	70.6	708	7	US-11-258-767-23 Sequence 23, Appl
22	48	70.6	708	7	US-11-258-767-24 Sequence 24, Appl
23	48	70.6	709	7	US-11-258-767-31 Sequence 31, Appl
24	48	70.6	710	7	US-11-258-767-33 Sequence 33, Appl
25	48	70.6	711	7	US-11-258-767-12 Sequence 12, Appl

26	48	70.6	711	7	US-11-258-767-15 Sequence 15, Appl
27	48	70.6	711	7	US-11-258-767-17 Sequence 17, Appl
28	48	70.6	711	7	US-11-258-767-18 Sequence 18, Appl
29	48	70.6	711	7	US-11-258-767-21 Sequence 21, Appl
30	48	70.6	711	7	US-11-258-767-27 Sequence 27, Appl
31	48	70.6	711	7	US-11-258-767-30 Sequence 30, Appl
32	48	70.6	711	7	US-11-258-767-34 Sequence 34, Appl
33	47	69.1	696	6	US-10-515-429-42 Sequence 34, Appl
34	45	66.2	677	6	US-10-515-429-39 Sequence 39, Appl
35	45	66.2	688	6	US-10-515-429-9 Sequence 40, Appl
36	45	66.2	707	7	US-11-258-767-14 Sequence 14, Appl
37	45	66.2	707	7	US-11-258-767-20 Sequence 20, Appl
38	40	58.8	414	6	US-10-471-571A-2756 Sequence 2756, Ap
39	37	54.4	47	6	US-10-515-429-26 Sequence 26, Appl
40	37	54.4	94	6	US-10-515-429-67 Sequence 67, Appl
41	37	54.4	118	6	US-10-370-959-111 Sequence 11, App
42	37	54.4	371	6	US-10-515-429-63 Sequence 63, Appl
43	37	54.4	618	6	US-10-471-571A-442 Sequence 442, App
44	36	52.9	131	6	US-10-471-571A-72 Sequence 72, Appl
45	36	52.9	691	6	US-10-471-571A-4786 Sequence 4786, Ap

ALIGNMENTS

RESULT 1
US-10-515-429-27
Sequence 27, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Turner, Christopher P.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515, 429
PRIOR FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406, 977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384, 060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485, 404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Transferrin
US-10-515-429-27
Query Match 100.0%; Score 68; DB 6; Length 49;
Best local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 YEKYLGEYKAV 13
Db 37 YEKYLGEYKAV 49
RESULT 2
US-10-515-429-3
Sequence 3, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun

;; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
;; FILE REFERENCE: 054710-5007-WO
;; CURRENT APPLICATION NUMBER: US/10/515,429
;; PRIOR FILING DATE: 2004-11-23
;; PRIOR APPLICATION NUMBER: PCT/US03/26779
;; PRIOR FILING DATE: 2003-08-26
;; PRIOR APPLICATION NUMBER: US 60/406,977
;; PRIOR FILING DATE: 2002-08-30
;; PRIOR APPLICATION NUMBER: US 10/384,060
;; PRIOR FILING DATE: 2002-03-10
;; PRIOR APPLICATION NUMBER: US 60/485,404
;; PRIOR FILING DATE: 2003-07-09
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 679
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Mature transferrin protein
US-10-515-429-3

Query Match 100.0%; Score 68; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 647 YEKYLGEYVKAV 659

RESULT 3
US-10-515-429-2
;; Sequence 2, Application US/10515429
;; Publication No. US20060105387A1
;; GENERAL INFORMATION:
;; APPLICANT: Prior, Christopher P.
;; APPLICANT: Turner, Andrew J.
;; APPLICANT: Sadeghi, Homayoun
;; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
;; FILE REFERENCE: 054710-5007-WO
;; CURRENT APPLICATION NUMBER: US/10/515,429
;; PRIOR FILING DATE: 2004-11-23
;; PRIOR APPLICATION NUMBER: PCT/US03/26779
;; PRIOR FILING DATE: 2003-08-26
;; PRIOR APPLICATION NUMBER: US 60/406,977
;; PRIOR FILING DATE: 2002-08-30
;; PRIOR APPLICATION NUMBER: US 10/384,060
;; PRIOR FILING DATE: 2003-03-10
;; PRIOR APPLICATION NUMBER: US 60/485,404
;; PRIOR FILING DATE: 2003-07-09
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 698
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-515-429-2

Query Match 100.0%; Score 68; DB 6; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 666 YEKYLGEYVKAV 678

RESULT 4
US-10-515-429-37
;; Sequence 37, Application US/10515429
;; Publication No. US20060105387A1
;; GENERAL INFORMATION:

;; APPLICANT: Prior, Christopher P.
;; APPLICANT: Turner, Andrew J.
;; APPLICANT: Sadeghi, Homayoun
;; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
;; FILE REFERENCE: 054710-5007-WO
;; CURRENT APPLICATION NUMBER: US/10/515,429
;; PRIOR FILING DATE: 2004-11-23
;; PRIOR APPLICATION NUMBER: PCT/US03/26779
;; PRIOR FILING DATE: 2003-08-26
;; PRIOR APPLICATION NUMBER: US 60/406,977
;; PRIOR FILING DATE: 2002-08-30
;; PRIOR APPLICATION NUMBER: US 10/384,060
;; PRIOR FILING DATE: 2003-03-10
;; PRIOR APPLICATION NUMBER: US 60/485,404
;; PRIOR FILING DATE: 2003-07-09
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 37
;; LENGTH: 676
;; TYPE: PRT
;; ORGANISM: Oryctolagus cuniculus
US-10-515-429-37

Query Match 85.3%; Score 58; DB 6; Length 676;
Best Local Similarity 76.9%; Pred. No. 0.015;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 644 YEKYLGDYIKAV 656

RESULT 5
US-11-258-767-36
;; Sequence 36, Application US/11258767
;; Publication No. US20060094082A1
;; GENERAL INFORMATION:
;; APPLICANT: Varadachary, Atul
;; APPLICANT: Glynn, Peter
;; APPLICANT: Petrak, Karel
;; APPLICANT: Engelmayr, Jose
;; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
;; FILE REFERENCE: HO-P02915US1
;; CURRENT APPLICATION NUMBER: US/11/258,767
;; PRIOR FILING DATE: 2005-10-26
;; PRIOR APPLICATION NUMBER: US 60/622,176
;; PRIOR FILING DATE: 2004-10-26
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 36
;; LENGTH: 686
;; TYPE: PRT
;; ORGANISM: PIG
US-11-258-767-36

Query Match 82.4%; Score 56; DB 7; Length 686;
Best Local Similarity 76.9%; Pred. No. 0.033;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 672 YEKYLGEYVTAI 684

RESULT 6
US-11-258-767-37
;; Sequence 37, Application US/11258767
;; Publication No. US20060094082A1
;; GENERAL INFORMATION:
;; APPLICANT: Varadachary, Atul
;; APPLICANT: Glynn, Peter
;; APPLICANT: Petrak, Karel
;; APPLICANT: Engelmayr, Jose

FILE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 37
LENGTH: 703
TYPE: PRT
ORGANISM: PIG
US-11-258-767-37

Query Match 82.4%; Score 56; DB 7; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.034;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
Db 671 YEKYLGEYVAV 683

RESULT 7
US-11-258-767-28
Sequence 28, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 28
LENGTH: 708
TYPE: PRT
ORGANISM: GOAT
US-11-258-767-28

Query Match 80.9%; Score 55; DB 7; Length 708;
Best Local Similarity 76.9%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
Db 676 YEKYLGEYVAV 688

RESULT 8
US-11-258-767-32
Sequence 32, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 32

LENGTH: 708
TYPE: PRT
ORGANISM: GOAT
US-11-258-767-32

Query Match 80.9%; Score 55; DB 7; Length 708;
Best Local Similarity 76.9%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
Db 676 YEKYLGEYVAV 688

RESULT 9
US-10-515-429-38
Sequence 38, Application US/10515429
Publication No. US20060105387A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-WO
CURRENT APPLICATION NUMBER: US/10/515,429
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/US03/26779
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/485,404
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 38
LENGTH: 676
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-515-429-38

Query Match 75.0%; Score 51; DB 6; Length 676;
Best Local Similarity 69.2%; Pred. No. 0.23;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
Db 644 YEKYLGEYVAV 656

RESULT 10
US-11-258-767-13
Sequence 13, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 13
LENGTH: 681
TYPE: PRT
ORGANISM: COW
US-11-258-767-13

Query Match 75.0%; Score 51; DB 7; Length 681;
Best Local Similarity 69.2%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 649 YEEYLGTEYVTAL 661

RESULT 11
US-11-258-767-25
; Sequence 25, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 698
; TYPE: PRT
; ORGANISM: RAT
US-11-258-767-25

Query Match 75.0%; Score 51; DB 7; Length 698;
Best Local Similarity 69.2%; Pred. No. 0.24;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 666 YEEYLGAEYLOAV 678

RESULT 12
US-11-258-767-16
; Sequence 16, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COW
US-11-258-767-16

Query Match 75.0%; Score 51; DB 7; Length 708;
Best Local Similarity 69.2%; Pred. No. 0.24;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 676 YEEYLGTEYVTAL 688

RESULT 13
US-11-258-767-19
; Sequence 19, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 708
; TYPE: PRT
; ORGANISM: WATER BUFFALO
US-11-258-767-19

Query Match 75.0%; Score 51; DB 7; Length 708;
Best Local Similarity 69.2%; Pred. No. 0.24;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 676 YEEYLGTEYVTAL 688

RESULT 14
US-11-258-767-22
; Sequence 22, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmayr, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 708
; TYPE: PRT
; ORGANISM: COW
US-11-258-767-22

Query Match 75.0%; Score 51; DB 7; Length 708;
Best Local Similarity 69.2%; Pred. No. 0.24;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 676 YEEYLGTEYVTAL 688

RESULT 15
US-11-258-767-29
; Sequence 29, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel

; APPLICANT: Engelmayr, Jose
 ; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
 ; FILE REFERENCE: HO-P02915US1
 ; CURRENT APPLICATION NUMBER: US/11/258,767
 ; CURRENT FILING DATE: 2005-10-26
 ; PRIOR APPLICATION NUMBER: US 60/622,176
 ; PRIOR FILING DATE: 2004-10-26
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 29
 ; LENGTH: 708
 ; TYPE: PRT
 ; ORGANISM: COM
 US-11-258-767-29

Query Match 75.0%; Score 51; DB 7; Length 708;
 Best Local Similarity 69.2%; Pred. No. 0.24;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YEKYLGEBYKAV 13
 Db 676 YEEYLGTEYVTAI 688

Search completed: June 13, 2006, 04:56:52
 Job time : 4.39706 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:02:32 ; Search time 194 Seconds
(without alignments)
30.638 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 1 YEKYLGEYVKAV 13
Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 34378

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	8	ADG46078 Human CDT
2	30	44.1	13	8	ADU07228 Human 4D4
3	30	44.1	13	8	ADT88295 Human IL-
4	30	44.1	13	9	AED66887 Human IL-
5	30	44.1	13	9	AED66959 Human IL-
6	28	41.2	13	2	AAW70384 Human reg
7	28	41.2	13	7	AEA79013 Bovine Se
8	26	38.2	13	7	ADW33519 HLA bindi
9	26	38.2	13	7	ADW34752 HLA bindi
10	25	36.8	13	2	AAW21308 Glucagon
11	25	36.8	13	2	AAW21301 Glucagon
12	25	36.8	13	2	AAW21313 Glucagon
13	25	36.8	13	8	ADP83124 Putative
14	25	36.8	13	8	ADU07237 Human 4D4
15	25	36.8	13	8	ADT88304 Human IL-
16	25	36.8	13	9	ADM39569 Human IL-
17	25	36.8	13	9	ADM39581 HMG CoA r
18	25	36.8	13	9	ADM39576 HMG CoA r
19	25	36.8	13	9	ADX26787 Putative
20	25	36.8	13	9	AED66896 Human IL-
21	25	36.8	13	10	AEF30609 Represent
22	25	36.8	13	10	AEF52225 Interfaci
23	25	36.8	13	10	AEF87217 Rat cytos

24	24	35.3	13	3	AAB39978 Anti-hiti1
25	24	35.3	13	5	ABJ10898 K+beta M6
26	24	35.3	13	7	ADM08910 Carline im
27	24	35.3	13	9	ADY64440 Human cyt
28	24	35.3	13	9	ADZ37854 Human kin
29	24	35.3	13	9	AEAS3802 Novel hum
30	24	35.3	13	9	AEAS5335 Novel hum
31	24	35.3	13	9	AEA44892 Apolipop
32	24	35.3	13	10	AEBS9361 Human pro
33	24	35.3	13	10	AEGB3146 CD200-spe
34	23	33.8	13	1	AAP82510 Viral inh
35	23	33.8	13	2	AAW21300 Glucagon
36	23	33.8	13	2	AAW21302 Glucagon
37	23	33.8	13	2	AAW21298 Glucagon
38	23	33.8	13	2	AAW21309 Glucagon
39	23	33.8	13	2	AAW21312 Glucagon
40	23	33.8	13	2	AAW21305 Glucagon
41	23	33.8	13	2	AAW21307 Glucagon
42	23	33.8	13	2	AAW21307 Glucagon
43	23	33.8	13	2	AAW21307 Glucagon
44	23	33.8	13	2	AAW61555 Biotinyl
45	23	33.8	13	2	AAW10774 Peptide u

ALIGNMENTS

RESULT 1
ID ADG46078 standard; peptide: 13 AA.
AC ADG46078;
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #4.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX Homo sapiens.
OS
XX
XX EPI378521-A1.
XX
XX 07-JAN-2004.
XX
XX 19-MAY-2003; 2003EP-00011334.
XX
XX 05-JUL-2002; 2002DE-01030550.
XX
XX (DADE-) DADE BEHRING WARBURG GMBH.
XX
XX Alchaus H;
XX
XX WPI; 2004-073743/08.
XX
XX New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
XX Claim 4; SEQ ID NO 4; 21pp; German.
XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences YVARSNGKEDLWELL, TTEDSIKIMNGEADAMSIDGCF, STLSNGSGLISFEN and
XX YEKYLGEYVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for

CC production of antibodies that specifically bind CDR from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDR, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDR in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDR peptide
CC fragments used in the method of the invention.

XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 68; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
Db 1 YEKYLGEYVKAV 13

RESULT 2
ADU07228
ID ADU07228 standard; peptide; 13 AA.
XX
AC ADU07228;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human 4D4 variable heavy chain (VH) CDR3.
XX
KW Respiratory infection; human; interleukin-9 antagonist; IL-9;
KW respiratory syncytial virus; anti-RSV antigen antibody;
KW leukotriene modifier; asthma-like symptom; wheezing; allergy;
KW immunomodulatory; anti-inflammatory; anti-viral; antibacterial; antifungal;
KW mast cell modulator; virucide; antibacterial; fungicide; antiaesthetic;
KW anti-allergic; 4D4 antibody; variable heavy chain; VH;
KW complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO2004091519-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004MO-US011329.
XX
PR 11-APR-2003; 2003US-0462307P.
XX
PR 10-JUN-2003; 2003US-0477801P.
XX
PA (MED1-) MEDIMUNE INC.
XX
PI Reed JL;
XX
XX WPI; 2004-775524/76.
XX
DR
XX
PT Managing, treating or ameliorating in a human subject a respiratory
PT infection or its symptoms caused by bacteria, fungi or respiratory
PT syncytial virus by administering an IL-9 antagonist.

XX
PS Disclosure; SEQ ID NO 3; 276pp; English.

XX
XX The invention relates to a method of managing, treating or ameliorating a
XX respiratory infection or its symptom in a human subject by administering a
XX an interleukin-9 (IL-9) antagonist. The method further comprises
XX administering to the subject an anti-respiratory syncytial virus (anti-
XX RSV) antigen antibody. The anti-RSV antigen antibody is palivizumab. The
XX method further comprises administering a leukotriene modifier, which is
XX montelukast, zafirlukast, pranlukast or zileuton. Also disclosed are: a
XX method of preventing the development, onset or progression of asthma or
XX one or more asthma-like symptoms in a child, a method of preventing,
XX managing, treating or ameliorating wheezing in a pre-term infant, infant
XX or child, a method of preventing, managing, treating or ameliorating
XX wheezing in a human subject, and a method of preventing, managing,
XX treating or ameliorating asthma or an allergy or its symptoms in a human

CC subject. Preventing the development, onset or progression of asthma or
CC one or more asthma-like symptoms in a child having or previously having a
CC respiratory infection comprises administering an IL-9 antagonist.
CC Preventing, managing, treating or ameliorating wheezing in a pre-term
CC infant, infant or child comprises administering an IL-9 antagonist. The
CC method further comprises administering at least one other therapy that is
CC not administration of an IL-9 antagonist. Preventing, managing, treating
CC or ameliorating wheezing in a human subject comprises administering an IL-
CC 9 antagonist and at least one other therapy that is not administration
CC of an IL-9 antagonist. The therapy is an immunomodulatory agent, an anti-
CC inflammatory agent, an anti-viral agent, an antibacterial, an antifungal
CC agent or a mast cell modulator. The method further comprises
CC administering to the subject a leukotriene modifier, an anti-histamine,
CC an anti-immunoglobulin E (IGE) antibody, an anti-IL-4 antibody or a mast
CC cell protease inhibitor. Preventing, managing, treating or ameliorating
CC asthma or an allergy or its symptoms in a human subject comprises
CC administering an IL-9 antagonist and at least one other asthma or allergy
CC therapy. The IL-9 antagonist is an antibody that immunospecifically binds
CC to an IL-9 receptor (IL-9R) or its subunit or to an IL-9 polypeptide. The
CC methods are useful in managing, treating or ameliorating in a human
CC subject a respiratory infection or its symptoms caused by bacteria, fungi
CC or RSV. This sequence represents a complementarity determining region
CC (CDR) region from human 4D4 antibody.

XX
SQ Sequence 13 AA;

Query Match 44.1%; Score 30; DB 8; Length 13;
Best Local Similarity 62.5%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
Db 3 YVGSIDYK 10

RESULT 3
ADT88295
ID ADT88295 standard; peptide; 13 AA.
XX
AC ADT88295;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human IL-19 antibody variable heavy domain CDR3 seqid 3.
XX
KW respiratory; antiinflammatory; immunosuppressive; antiaesthetic;
KW anti-allergic; antiarthritic; neuroprotective; antineurotic; immunotoxin;
KW angiogenesis inhibitor; TNF alpha antagonist; IL-9 antagonist; IL-9;
KW IL-9 antibody; 4D4; 4D4 H2-1 D11; 4D4com-XF9; 4D4com-2F9; 7F3; 71A10;
KW 22D3; 7F3com-2H2; 7F3com-3H5; 7F3com-3D4; IL-9 associated disorder;
KW respiratory infection; respiratory syncytial virus; parainfluenza virus;
KW human metapneumovirus; inflammatory disorder; asthma; allergy; arthritis;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW variable heavy domain; complementarity determining region 3; CDR3.
XX
OS Homo sapiens.
XX
PN WO2004091510-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004MO-US011172.
XX
PR 11-APR-2003; 2003US-0462259P.
XX
PR 10-JUN-2003; 2003US-0477977P.
XX
PA (MED1-) MEDIMUNE INC.
XX
PI Reed JL;
XX
XX WPI; 2004-775520/76.
XX
DR
XX
PT New IL-9 antibody comprising a variable heavy or light domain or a

PT complementarity determining region having an amino acid sequence of e.g.,
PT 4D4, useful in treating or preventing e.g., respiratory infection or
PT inflammatory disorder.
XX
XX
XX Disclosure; SEQ ID NO 3; 291pp; English.
PS
CC The invention describes a new IL-9 antibody comprising: a variable heavy
CC (VH) or variable light (VL) domain having an amino acid sequence of the
CC VH or VL domain of 4D4, 4D4 H2-1 D11, 4D4com-3H5, 4D4com-2F9, 7F3, 71A10,
CC 22D3, 7F3com-2H2, 7F3com-3H5 or 7F3com-3D4; or a complementarity
CC determining region (CDR) having an amino acid sequence of a CDR of 4D4,
CC 4D4 H2-1 D11, 4D4com-3H5, 4D4com-2F9, 7F3, 71A10, 22D3, 7F3com-2H2,
CC 7F3com-3H5 or 7F3com-3D4. The antibody immunospecifically binds to a
CC human IL-9 polypeptide. Also described are: a pharmaceutical composition
CC comprising the IL-9 antibody and a carrier; a method for preventing,
CC treating, managing or ameliorating a disease or disorder characterized by
CC aberrant expression or activity of an IL-9 polypeptide or an IL-9R; a
CC method of diagnosing, prognosing, or monitoring a disorder or disease
CC characterised by aberrant expression or activity of an IL-9 polypeptide
CC or aberrant expression or activity of an IL-9R; a kit comprising the
CC antibody and instructions for use, in one or more containers; and an
CC article of manufacture comprising a packaging material and a
CC pharmaceutical agent contained within the packaging material, where the
CC pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9
CC antibody is useful in preparing a composition for diagnosing, treating or
CC preventing a disease or disorder characterised by aberrant expression or
CC activity of an IL-9 polypeptide or an IL-9R, e.g., respiratory infection
CC caused by bacteria or respiratory syncytial virus, parainfluenza virus or
CC human metapneumovirus, inflammatory disorder such as asthma, allergy or
CC arthritis or autoimmune disorder such as rheumatoid arthritis and
CC multiple sclerosis. This is the amino acid sequence of a human IL-9
CC (CDR3).
CC
XX
SQ Sequence 13 AA;
Qy
Best Local Similarity 44.1%; Score 30; DB 8; Length 13;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 4 YLGEYVK 11
3 YGSDYVK 10
DE Human IL-9 antibody, 4D4 H2-1 D11 VH domain CDR3 peptide, SEQ ID: 3 #1.
XX
XX Gene therapy; chemotherapy; animal disease model; inflammation;
XX antiinflammatory; asthma; antiasthmatic; allergy; antiallergic;
XX autoimmune disease; immunosuppressive; diabetes; antidiabetic;
XX haemolysis disease; antithyroid; adrenal disease; endocrine-gen.; anemia;
XX antianemic; multiple sclerosis; neuroprotective; rheumatoid arthritis;
XX antirheumatic; antirheumatic; systemic lupus erythematosus;
XX dermatological; carditis; cardiant; Sjogrens syndrome; polymyositis;
XX muscular-gen.; dermatomyositis; scleroderma; hyperproliferation;
XX cytosarctic; infection; antimicrobial; respiratory tract infection;
XX respiratory-gen.; interleukin-9; cytokine; lymphokines; antibody;
XX heavy chain variable region; 4D4 H2-1 D11; 7F3; 71A10; 7F3 22D3;
XX 7F3com-2H2; 7F3com-3H5; 7F3com-3D4.
XX Homo sapiens.
OS
PN US2005260204-A1.
XX
XX 24-NOV-2005.
PD

XX
XX 12-APR-2005; 2005US-00105268.
PF
XX
XX 12-APR-2004; 2004US-0561845P.
PR
XX
XX (MEDI-) MEDIMMUNE INC.
PA
XX
XX Allan CB;
XX WPI; 2005-796072/81.
DR N-PSDB; AED66930.
PT
XX New antibody formulation comprises antibody or antibody fragment that
XX immunospecifically binds to an IL-9 polypeptide, useful for preventing,
XX managing, treating, or ameliorating, e.g. asthma, allergy, diabetes, or
XX multiple sclerosis.
XX
XX Disclosure; SEQ ID NO 3; 125pp; English.
PS
XX The present invention provides liquid formulation of antibodies or
XX antibody fragments that immunospecifically binds to an interleukin-9 (IL-
XX 9) polypeptide. The formulation exhibit stability, low to undetectable
XX levels of aggregation and very little to no loss of the biological
XX activities of antibodies and its fragments, even during the long period
XX of storage. The antibody formulation of the invention is useful for
XX preventing, managing, treating or ameliorating a disease or disorder
XX associated with aberrant expression and/or activity of an IL-9
XX polypeptide, IL-9R or one or more subunits, inflammatory disorders such
XX as asthma or an allergy, autoimmune disorders such as diabetes,
XX Hashimoto's disease, autoimmune adrenal insufficiency, pure red cell
XX anemia, multiple sclerosis, rheumatoid arthritis, systemic lupus
XX erythematosus, rheumatoid arthritis, chronic inflammation, Sjogren's
XX syndrome polymyositis, dermatomyositis or scleroderma, proliferative
XX disease or an infection (preferably, a respiratory infection). The
XX invention is also useful in gene therapy, chemotherapy and to generate
XX animal disease models. The present sequence is a heavy chain variable
XX (VH) domain complementarity determining region, CDR3 peptide present in
XX human interleukin-9 (IL-9) antibodies 4D4 H2-1 D11, 7F3, 71A10, 7F3 22D3,
XX 7F3com-2H2, 7F3com-3H5 and 7F3com-3D4. Note: The present sequence is the
XX SEQ ID NO: 3 which is given in the sequence listing. This sequence
XX differs from the SEQ ID NO: 3 shown on table 1 in page 2 (antibody 4D4)
XX in the disclosure of the specification (see AED66930).
XX
SQ Sequence 13 AA;
Qy
Best Local Similarity 44.1%; Score 30; DB 9; Length 13;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 4 YLGEYVK 11
3 YGSDYVK 10
DE Human IL-9 antibody, 4D4 VH domain CDR3 peptide, SEQ ID: 3 #2.
XX
XX Gene therapy; chemotherapy; animal disease model; inflammation;
XX antiinflammatory; asthma; antiasthmatic; allergy; antiallergic;
XX autoimmune disease; immunosuppressive; diabetes; antidiabetic;
XX haemolysis disease; antithyroid; adrenal disease; endocrine-gen.; anemia;
XX antianemic; multiple sclerosis; neuroprotective; rheumatoid arthritis;
XX antirheumatic; antirheumatic; systemic lupus erythematosus;
XX dermatological; carditis; cardiant; Sjogrens syndrome; polymyositis;
XX muscular-gen.; dermatomyositis; scleroderma; hyperproliferation;
XX cytosarctic; infection; antimicrobial; respiratory tract infection;
XX

KW respiratory-gen.; interleukin-9; cytokine; lymphokine; antibody;
KM heavy chain variable region; 4D4 H2-1 D11; 7F3; 71A10; 7F3 22D3;
XX 7F3com-2H2; 7F3com-3H5; 7F3com-3D4.
XX
OS Homo sapiens.
XX
PN US2005260204-A1.
XX
PD 24-NOV-2005.
XX
PF 12-APR-2005; 2005US-00105268.
XX
PR 12-APR-2004; 2004US-0561845P.
XX
PA (MED1-) MEDIMUNE INC.
XX
PI Allan CB;
XX
DR WPI; 2005-796072/81.
XX
PT New antibody formulation comprises antibody or antibody fragment that
PT immunospecifically binds to an IL-9 polypeptide, useful for preventing,
PT managing, treating, or ameliorating, e.g. asthma, allergy, diabetes, or
PT multiple sclerosis.
XX
PS Disclosure; SEQ ID NO 3; 125pp; English.
XX
CC The present invention provides liquid formulation of antibodies or
CC antibody fragments that immunospecifically binds to an interleukin-9 (IL-
CC 9) polypeptide. The formulation exhibit stability, low to undetectable
CC levels of aggregation and very little to no loss of the biological
CC activities of antibodies and its fragments, even during the long period
CC of storage. The antibody formulation of the invention is useful for
CC preventing, managing, treating or ameliorating a disease or disorder
CC associated with aberrant expression and/or activity of an IL-9
CC polypeptide, IL-9R or one or more subunits, inflammatory disorders such
CC as asthma or an allergy, autoimmune disorders such as diabetes,
CC Hashimoto's disease, autoimmune adrenal insufficiency, pure red cell
CC anemia, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, rheumatoid arthritis, chronic inflammation, Sjogren's
CC syndrome polymyositis, dermatomyositis or scleroderma, proliferative
CC disease or an infection (preferably, a respiratory infection). The
CC invention is also useful in gene therapy, chemotherapy and to generate
CC animal disease models. The present sequence is a heavy chain variable
CC (VH) domain complementarily determining region, CDR3 peptide present in
CC human Interleukin-9 (IL-9) antibody 4D4. Note: The present sequence is
CC the SEQ ID NO: 3 shown on table 1 in page 2 in disclosure of the
CC specification. This sequence differs from the SEQ ID NO: 3 given in the
CC sequence listing of the specification (4D4 H2-1 D11, 7F3, 71A10, 7F3
CC 22D3, 7F3com-2H2, 7F3com-3H5 and 7F3com-3D4) (see AED66887).
XX
SQ Sequence 13 AA;
XX
Query Match 44.1%; Score 30; DB 9; Length 13;
Best Local Similarity 62.5%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4 YIGGEYVK 11
| | : |||
| | : |||
Db 3 YYGSDYVK 10
XX
RESULT 6
AAW70384 ID AAW70384 standard; protein; 13 AA.
XX
AC AAW70384;
XX
DT 02-DEC-1998 (first entry)
XX
DE human regeneration-associated serpin-1 peptide.
XX
KW Human; regeneration-associated serpin-1 protein; RASP-1; liver disorder;

KW viral infection; hepatitis; cirrhosis; transplantation;
KM hepatocyte growth factor; HGF.
XX
OS Homo sapiens.
XX
PN WO9833890-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US001962.
XX
PR 03-FEB-1997; 97US-0036842P.
XX
PA (HEPA-) HEPATIX INC.
XX
PI Purchio AF;
XX
DR WPI; 1998-446810/38.
XX
PT New isolated human regeneration-associated serpin-1 - used to develop
PT products for the diagnosis and treatment of liver conditions, e.g. viral
PT infection, autoimmunity, hepatitis or cirrhosis.
XX
PS Example 1; Page 27; 40pp; English.
XX
CC This is the amino acid sequence of the human regeneration-associated
CC serpin-1 peptide (RASP-1), used in the method of the invention to develop
CC products for the diagnosis and treatment of liver conditions. The RASP-1
CC polypeptides are involved in regeneration of the liver and are useful in
CC the diagnosis, prognosis and treatment of liver-associated disorders,
CC such as viral infection, autoimmunity, hepatitis or cirrhosis. They can
CC also be used in methods for maintaining cultured cells or tissues, such
CC as hepatocytes cells or tissues, prior to transplantation. In addition,
CC RASP-1, can be used to promote hepatocyte growth in vitro, in order to,
CC e.g. facilitate production of growth factors, such as hepatocyte growth
CC factor (HGF), that are produced by them. The regulatory region of RASP-1
CC allows tissue-specific expression (i.e. liver) of an operatively linked
CC gene
XX
SQ Sequence 13 AA;
XX
Query Match 41.2%; Score 28; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 YERYLGEYV 9
| | : |||
| | : |||
Db 4 YENQIWEYV 12
XX
RESULT 7
AEA79013 ID AEA79013 standard; peptide; 13 AA.
XX
AC AEA79013;
XX
DT 11-AUG-2005 (first entry)
XX
DE Bovine Serum Albumin indexed peptide database peptide #229.
XX
KM mass spectrometry; peptide index; protein identification;
KM protein quantitation; protease; high-resolution mass spectrometry;
KM proteomics; genomics; bioinformatics; Bovine Serum Albumin.
XX
OS Bos sp.
XX
PN WO2003054549-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-GB005571.
XX
PR 08-DEC-2001; 2001US-0340460P.

PR 14-MAR-2002; 2002US-0364847P.
XX
XX (MICR-) MICROMASS LTD.
PA
XX Geromanos S, Dongre A, Opitcheck G, Silva J;
PI
XX WPI; 2003-569290/53.
DR
XX
XX A method of mass spectrometry, useful in protein identification and
PT quantitation, by mass analyzing the first molecules in the first mixture
PT and accurately determining the mass to charge ratio of the first
PT molecules in the first mixture.
XX
XX
PS Disclosure; Fig 9H; 123pp; English.
XX
XX The invention relates to a novel method of mass spectrometry. The method
CC comprises mass analyzing the first molecules in a first mixture and
CC accurately determining the mass to charge ratio of the first molecules in
CC the first mixture. The invention further relates to: generating an index
CC for use in identifying molecules of biological origin by mass
CC spectrometry by accurately determining the masses or mass to charge
CC ratios of molecules comprising peptides resulting from the digestion or
CC fragmentation of a polypeptide or protein; determining a first physico-
CC chemical property other than mass or mass to charge ratio of the
CC molecules comprising peptides; and optionally determining a second,
CC third, fourth and/or fifth physico-chemical property of the molecules
CC comprising peptides; and a mass spectrometer comprising a mass analyzer
CC for accurately determining the mass to charge ratio of the first
CC molecules, and means for identifying the first molecules of the basis of
CC at least the first physico-chemical property and the accurately
CC determined mass to charge ratio of the first molecules and optionally on
CC the basis of the second, third, fourth and/or fifth physico-chemical
CC property. The method and spectrometer are useful in protein
CC identification, protein quantitation, proteases, high-resolution mass
CC spectrometry, proteomics, genomics and bioinformatics. This sequence
CC represents a peptide from an indexed peptide database created by the
CC novel mass spectrometry method of the invention.
XX
SQ Sequence 13 AA;
Query Match 41.2%; Score 28; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 LGEEYV 10
: |||:
: |||:
Db 1 IGEYI 6
RESULT 8
ADM33519
ID ADM33519 standard; peptide; 13 AA.
XX
AC ADM33519;
XX
DT 10-MAR-2005 (first entry)
XX
DE HLA binding epitope #4269.
XX
XX
KM Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KM viral disease; cancer.
XX
OS Unidentified.
XX
PN WO2003040165-A2.
XX
PD 15-MAY-2003.
XX
PF 18-OCT-2001; 2001WO-US051650.
XX
PR 19-OCT-2000; 2000US-0242350P.
XX
PR 20-APR-2001; 2001US-0285624P.
XX

XX
XX (EPIM-) EPIMMUNE INC.
PA
XX Sette A, Sidney J, Southwood S;
PI
XX WPI; 2003-441519/41.
DR
XX
XX New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.
XX
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
XX The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in Tables 2-31.
XX
SQ Sequence 13 AA;
Query Match 38.2%; Score 26; DB 7; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 3 KYLGEYVK 11
|||: : |||:
|||: : |||:
Db 2 KYVKQNYLK 10
RESULT 9
ADM34752
ID ADM34752 standard; peptide; 13 AA.
XX
AC ADM34752;
XX
DT 10-MAR-2005 (first entry)
XX
DE HLA binding epitope #5502.
XX
XX
KM Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KM viral disease; cancer.
XX
OS Unidentified.
XX
PN WO2003040165-A2.
XX
PD 15-MAY-2003.
XX
PF 18-OCT-2001; 2001WO-US051650.
XX
PR 19-OCT-2000; 2000US-0242350P.
XX
PR 20-APR-2001; 2001US-0285624P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
XX WPI; 2003-441519/41.
XX

PT New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.
XX
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
CC ADM37745 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 13 AA:
Query Match 38.2%; Score 26; DB 7; Length 13;
Best Local Similarity 44.4%; Pred. No. 2,7e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 3 KYIGEEYVK 11
| | | | |
Db 2 KYVKQNYLK 10
RESULT 10
AAW21308
ID AAW21308 standard; peptide; 13 AA.
XX
AC AAW21308;
XX
DT 29-JUL-1997 (first entry)
XX
DE Glucagon precursor derived signal oligopeptide #13.
XX
KM Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; STV;
KM competitive inhibitor; feedback regulator; synthetase; gastrin precursor;
KM charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KM hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rheus;
KM gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KM Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KM apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KM herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KM Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KM fibroblast MMP1; schistosoma elastase precursor; schistosomlin;
KM hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX
OS Homo sapiens.
XX
PN WO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US000575.
XX
PR 14-JAN-1994; 94US-00182248.
XX
PA (RATH/) RATH M.
XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).
XX
XX
PS Claim 5; Page 40; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localized on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 13 AA:
Query Match 36.8%; Score 25; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 3.9e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 YEKYIGEEYVK 11
| | | | |
Db 2 YSKYLDNRRAK 12
RESULT 11
AAW21301
ID AAW21301 standard; peptide; 13 AA.
XX
AC AAW21301;
XX
DT 29-JUL-1997 (first entry)
XX
DE Glucagon precursor derived signal oligopeptide #6.
XX
KM Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; STV;
KM competitive inhibitor; feedback regulator; synthetase; gastrin precursor;
KM charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KM hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rheus;
KM gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KM Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KM apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KM herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KM Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KM fibroblast MMP1; schistosoma elastase precursor; schistosomlin;
KM hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX
OS Homo sapiens.
XX
PN WO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US000575.
XX
PR 14-JAN-1994; 94US-00182248.
XX
PA (RATH/) RATH M.
XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as

PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).
PS Claim 5; Page 39; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 13 AA;
Query Match 36.8%; Score 25; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 3.9e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 YEKYIGEEYVK 11
| | | | |
Db 2 YSKYLDNRRAK 12
RESULT 12
AAW21313
ID AAW21313 standard; peptide; 13 AA.
XX
AC AAW21313;
XX
DT 29-JUL-1997 (first entry)
XX
DE Glucagon precursor derived signal oligopeptide #18.
XX
KM Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; STV;
KM competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KM charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KM hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KM gonadotrophin precursor; plasminogen activator inhibitor 2; prorenin;
KM Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KM apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KM herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A1;
KM Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KM fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KM hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX
OS Homo sapiens.
XX
PN MO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US000575.
XX
PR 14-JAN-1994; 94US-00182248.
XX
PA (RATH/) RATH M.
XX
PI RATH M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between

PT protein(s).
PS Claim 5; Page 41; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 13 AA;
Query Match 36.8%; Score 25; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 3.9e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 YEKYIGEEYVK 11
| | | | |
Db 2 YSKYLDNRRTK 12
RESULT 13
ADP83124
ID ADP83124 standard; peptide; 13 AA.
XX
AC ADP83124;
XX
DT 23-SEP-2004 (first entry)
XX
DE Putative fat-like cadherin precursor FGFR binding motif peptide SEQ:32.
XX
KM protein interaction modulation; cell-surface receptor;
KM receptor binding site; neuroprotective; vulnerability; antidiabetic;
KM neoplastic; gene therapy; fibroblast growth factor receptor; FGFR;
KM receptor ligand; neural cell adhesion molecule; NCAM; solid tumour;
KM neoplasia; central nervous system disorder;
KM peripheral nervous system disorder; postoperative nerve damage;
KM traumatic nerve damage; impaired myelination; post-ischaemic damage;
KM stroke; Parkinson's disease; Alzheimer's disease; Huntington's disease;
KM dementia; multifactorial dementia; sclerosis; nerve degeneration;
KM diabetes mellitus; schizophrenia; mood disorder; manic depression;
KM neuro-muscular connection; organ transplantation;
KM genetic atrophic muscle disorder; traumatic atrophic muscle disorder;
KM degenerative condition; acute myocardial infarction; angiogenesis;
KM wound-healing; revascularisation.
XX
OS Synthetic.
XX
PN WO2004056865-A2.
XX
PD 08-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-DK000901.
XX
PR 20-DEC-2002; 2002DK-00001982.
XX
PR 03-MAR-2003; 2003DK-00000330.
XX
PA (ENKA-) ENKAM PHARM AS.
XX
PI Berezin V, Albrechtsen M, Bock E;
XX
DR WPI; 2004-517671/49.

XX Modulating the interaction between at least two different proteins by
PT providing a compound capable of interfering with the receptor and the
PT polypeptide interaction and presenting the compound to the different
PT proteins.
XX
XX Claim 45; SEQ ID NO 32; 154pp; English.
XX
XX The present invention describes a method for modulating the interaction
CC between at least two different proteins, where one of the proteins is
CC represented by a functional cell-surface receptor, or its fragment or
CC variant or by a polypeptide having a binding site to the receptor, where
CC at least a part of the binding site comprises at least one of the
CC sequences given in SEQ ID NO:1 to 146 (ADP83093 to ADP83238), or
CC fragments, or variants, or homologues of the sequences, or fragments or
CC variants of the homologues, comprising (i) providing a compound capable
CC of interacting with the receptor and/or polypeptide to interfere with the
CC receptor and the polypeptide interaction, and (ii) presenting the
CC compound of step (i) to at least two different proteins. The compound has
CC neuroprotective, vulnerary, antidiabetic and nephroprotective activities, and
CC can be used in gene therapy. The method is useful in modulating the
CC interaction between at least two different proteins, where one of the
CC proteins is represented by a functional cell-surface receptor, selected
CC from the family of fibroblast growth factor receptors (FGFRs), and the
CC other protein is the receptor ligand, can be used for treating normal,
CC degenerated or damaged neural cell adhesion molecule (NCAM) presenting
CC cells; solid tumour requiring neoangiogenesis, diseases and conditions of
CC the central and peripheral nervous system, of the muscles or of various
CC organs, e.g., postoperative nerve damage, traumatic nerve damage,
CC impaired myelination of nerve fibres, post-ischaemic damage, e.g.,
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC Huntington's disease, dementias such as multi-infarct dementia, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission, and schizophrenia,
CC mood disorders, such as manic depression, diseases or conditions of the
CC muscles including conditions with impaired function of neuro-muscular
CC connections, such as after organ transplantation, or such as genetic or
CC traumatic atrophic muscle disorders; degenerative conditions of the
CC gonads, of the pancreas such as diabetes mellitus type I and II, of the
CC kidney such as nephrosis or of the heart, liver and bowel; for preventing
CC cell death of heart muscle cells, such as after acute myocardial
CC infarction, or after angiogenesis; for promoting wound-healing; for
CC revascularisation; or for stimulating the ability to learn and/or the
CC short and/or long-term memory.
XX
XX Sequence 13 AA;
SQ
Query Match 36.8%; Score 25; DB 8; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 2 EKYLGEEYVK 11
Db 3 ENSLGKTVAK 12
RESULT 14
ADU07237
ID ADU07237 standard; peptide; 13 AA.
XX
XX ADU07237;
AC 13-JAN-2005 (first entry)
XX
XX Human 4D4com-XF-9 variable heavy chain (VH) CDR3.
DE
XX Respiratory infection; human; interleukin-9 antagonist; IL-9;
XX respiratory syncytial virus; anti-RSV antigen antibody;
KW leukotriene modifier; asthma-like symptom; wheezing; allergy;

KW immunomodulatory; anti-inflammatory; anti-viral; antibiotic; antifungal;
KW mast cell modulator; virocid; antibacterial; fungicide; antiseptic;
KW anti-allergic; 4D4com-XF-9 antibody; variable heavy chain; VH;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO2004091519-A2.
PN
XX 28-OCT-2004.
PD
XX
XX 12-APR-2004; 2004MO-US011329.
PF
XX
XX 11-APR-2003; 2003US-0462307P.
PR
XX 10-JUN-2003; 2003US-0477801P.
PR
XX (MEDI-) MEDIMUNE INC.
PA
XX Reed JL;
PI
XX WPI; 2004-775524/76.
DR
XX
XX Managing, treating or ameliorating in a human subject a respiratory
PT infection or its symptoms caused by bacteria, fungi or respiratory
PT syncytial virus by administering an IL-9 antagonist.
XX
XX Disclosure; SEQ ID NO 12; 276pp; English.
PS
XX
XX The invention relates to a method of managing, treating or ameliorating a
CC respiratory infection or its symptom in a human subject by administering
CC an interleukin-9 (IL-9) antagonist. The method further comprises
CC administering to the subject an anti-respiratory syncytial virus (anti-
CC RSV) antigen antibody. The anti-RSV antigen antibody is palivizumab. The
CC method further comprises administering a leukotriene modifier, which is
CC montelukast, zafirlukast, pranlukast or zileuton. Also disclosed are: a
CC method of preventing the development, onset or progression of asthma or
CC one or more asthma-like symptoms in a child, a method of preventing,
CC managing, treating or ameliorating wheezing in a pre-term infant, infant
CC or child, a method of preventing, managing, treating or ameliorating
CC wheezing in a human subject, and a method of preventing, managing,
CC treating or ameliorating asthma or an allergy or its symptoms in a human
CC subject. Preventing the development, onset or progression of asthma or
CC one or more asthma-like symptoms in a child having or previously having a
CC respiratory infection comprises administering an IL-9 antagonist.
CC Preventing managing, treating or ameliorating wheezing in a pre-term
CC infant, infant or child comprises administering an IL-9 antagonist. The
CC method further comprises administering at least one other therapy that is
CC not administration of an IL-9 antagonist. Preventing, managing, treating
CC or ameliorating wheezing in a human subject comprises administering an IL-
CC -9 antagonist and at least one other therapy that is not administration
CC of an IL-9 antagonist. The therapy is an immunomodulatory agent, an anti-
CC inflammatory agent, an anti-viral agent, an antibiotic, an antifungal
CC agent or a mast cell modulator. The method further comprises
CC administering to the subject a leukotriene modifier, an anti-histamine,
CC an anti-immunoglobulin E (IgE) antibody, an anti-IL-4 antibody or a mast
CC cell protease inhibitor. Preventing, managing, treating or ameliorating
CC asthma or an allergy or its symptoms in a human subject comprises
CC administering an IL-9 antagonist and at least one other asthma or allergy
CC therapy. The IL-9 antagonist is an antibody that immunospecifically binds
CC to an IL-9 receptor (IL-9R) or its subunit or to an IL-9 polypeptide. The
CC methods are useful in managing, treating or ameliorating in a human
CC subject a respiratory infection or its symptoms caused by bacteria, fungi
CC or RSV. This sequence represents a complementarity determining region
CC (CDR) region from human 4D4com-XF-9 antibody.
XX
XX Sequence 13 AA;
SQ
Query Match 36.8%; Score 25; DB 8; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 4 YLGEYEVK 11
| : : |

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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:06:17 ; Search time 38 Seconds
(without alignments)

32.916 Million cell updates/sec

Title: US-10-612-162A-4

Perfect score: 68

Sequence: 1 YEKYLGEHYKAV 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	38.2	13	2	PH1479
2	20	29.4	13	2	S47359
3	20	29.4	13	2	S47361
4	20	29.4	13	2	S47365
5	20	29.4	13	2	S47368
6	20	29.4	13	2	S47372
7	20	29.4	13	2	S47383
8	20	29.4	13	2	S47384
9	20	29.4	13	2	S47374
10	19	27.9	13	2	E60396
11	18	26.5	13	2	A32734
12	18	26.5	13	2	G44644
13	17	25.0	13	2	PT0263
14	17	25.0	13	2	PT0290
15	17	25.0	13	2	S47373
16	16	23.5	13	2	A33208
17	16	23.5	13	2	E53275
18	16	23.5	13	2	S14316
19	16	23.5	13	2	S32473
20	15	22.1	13	2	A53608
21	15	22.1	13	2	S47380
22	14	20.6	13	1	UNBO
23	14	20.6	13	2	A54326
24	14	20.6	13	2	S47388
25	14	20.6	13	2	S47389
26	14	20.6	13	2	PH1585
27	14	20.6	13	2	PH0788
28	14	20.6	13	2	PH0168
29	14	20.6	13	2	S66558

30	13	19.1	13	2	A28953	alpha-conotoxin SI
31	13	19.1	13	2	S39413	tubulin beta chain
32	13	19.1	13	2	S01119	photosystem II pro
33	13	19.1	13	2	B26093	microbial collagen
34	13	19.1	13	2	PA0031	protein QA00045 -
35	13	19.1	13	2	A33660	osteoclast functio
36	13	19.1	13	2	S65612	tubulin alpha-chain
37	13	19.1	13	2	B20907	ig kappa-1 chain J
38	13	19.1	13	2	PH1593	ig H chain V-D-J r
39	13	19.1	13	2	PH1596	ig H chain V-D-J r
40	13	19.1	13	2	PH0787	T-cell receptor al
41	13	19.1	13	2	PH0928	T-cell receptor be
42	13	19.1	13	2	A32453	phloroglucinol red
43	13	19.1	13	2	G22565	R-phycocerythrin ga
44	13	19.1	13	2	C61576	ribosomal protein
45	12	17.6	13	2	A44818	extracellular lipa

ALIGNMENTS

RESULT 1
PH1479
T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C/Accession: PH1479
R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A>Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:91171821; PMID:8436911
A/Accession: PH1479
A/Molecule type: mRNA
A/Residues: 1-13 <CAS>
A/Cross-references: UNIPARC:UPI00017C79F
A/Experimental source: cytolytic T-lymphocyte
C/Keywords: receptor; T-cell

Query Match
Best Local Similarity 38.2%; Score 26; DB 2; Length 13;
Matches 4; Conservativity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservativity 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLG 6
DB 8 YEQYFG 13

RESULT 2

S47359
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47359
R/Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0101 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47359
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI000116679; EMBL:Z35683; NID:G527455; PIDN:CAA84752.1; PI
C/Keywords: T-cell receptor

Query Match
Best Local Similarity 29.4%; Score 20; DB 2; Length 13;
Matches 3; Conservativity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
DB 9 YEQY 12

RESULT 3

S47361
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47361
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47361
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI000011667B; EMBL:Z35685; NID:G527459; PIDN:CAA84754.1; PI
C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 4

S47365
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47365; S47375; S47379; S47396; S47397; S47358; S47355
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47365
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35690; NID:G527471; PIDN:CAA84759.1; PI
A/Accession: S47375
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE2>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35700; NID:G527493; PIDN:CAA84769.1; PI
A/Accession: S47379
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE3>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35708; NID:G527509; PIDN:CAA84777.1; PI
A/Accession: S47396
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE4>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35674; NID:G527527; PIDN:CAA84743.1; PI
A/Accession: S47397
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE5>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35675; NID:G527529; PIDN:CAA84744.1; PI
A/Accession: S47398
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE6>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

Db 9 YEQY 12

RESULT 5

S47368
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47368
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47368
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116681; EMBL:Z35693; NID:G527477; PIDN:CAA84762.1; PI
C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 6

S47372
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47372
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47372
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116684; EMBL:Z35697; NID:G527485; PIDN:CAA84766.1; PI
C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 7

S47383
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47383
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47383
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116680; EMBL:Z35709; NID:G527513; PIDN:CAA84778.1; PI
C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 8

S47384

T-cell antigen receptor VJ junction beta chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C/Accession: S47384

R/Lehner, P.J.

Submitted to the EMBL Data Library, August 1994

A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A/Reference number: S47355

A/Accession: S47384

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-13 <LEH>

A/Cross-references: UNIPARC:UPI0000116689; EMBL:Z35704; NID:G527501; PIDN:CAA84773.1; PI

C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 9

S47374

T-cell antigen receptor VJ junction beta chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999

C/Accession: S47374; S47399; S47364

R/Lehner, P.J.

Submitted to the EMBL Data Library, August 1994

A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A/Reference number: S47355

A/Accession: S47374

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-13 <LEH>

A/Cross-references: UNIPARC:UPI0000116674; EMBL:Z35699; NID:G527491; PIDN:CAA84768.1; PI

A/Accession: S47399

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-13 <LEZ>

A/Cross-references: UNIPARC:UPI0000116674; EMBL:Z35677; NID:G527533; PIDN:CAA84746.1; PI

C/Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 10

E60396

antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)

C/Species: Plasmodium falciparum

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000

C/Accession: E60396

R/Limpitboon, T.; Taylor, D.W.; Jones, G.; Geyssen, H.M.; Saul, A.

Southeast Asian J. Trop. Med. Public Health 21, 388-396, 1990
A/Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclonal

A/Reference number: A60396; MUID:91164876; PMID:1706114

A/Accession: E60396

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-13 <LIM>

A/Cross-references: UNIPARC:UPI000017B5EF; GB:M31305

Query Match 27.9%; Score 19; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 5.2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YLGEHYK 11
||:|
Db 1 FLKSEPMK 8

RESULT 11

A32734

enkephalin precursor - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004

C/Accession: A32734

R/Micanovic, R.; Ray, P.; Kungel, W.; Lewis, R.V.

Biochem. Biophys. Res. Commun. 118, 299-303, 1984

A/Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin

A/Reference number: A32734; MUID:84128045; PMID:6546517

A/Accession: A32734

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <MIC>

A/Cross-references: UNIPROT:Q7M2Z6; UNIPARC:UPI00001765B8

C/Superfamily: proenkephalin

C/Keywords: neuropeptide; opioid peptide

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LGREY 9
||:|
Db 5 LGKRY 9

RESULT 12

G44644

neurotoxin-associated protein type B Hn+ 35K chain, band 3b - Clostridium botulinum (fra

C/Species: Clostridium botulinum

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: G44644

R/Somers, B.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A/Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he

A/Reference number: A44644; MUID:92143938; PMID:1761887

A/Accession: G44644

A/Contents: type B

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <SOM>

A/Cross-references: UNIPROT:Q9RSN5; UNIPARC:UPI0000089879

A/Note: sequence extracted from NCBI backbone (NCBIP:83785)

C/Keywords: hemagglutinin

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEKYLGREYV 10
||:|
Db 4 YQNLINDKIV 13

RESULT 13

PT0263
Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0263
R:Yamada, M.; Maeserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0263
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Cross-references: UNIPARC:UPI000017C1F0
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match

25.0%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 YLG 6
111
Db 9 YLG 11

RESULT 14

PT0290
Ig heavy chain CRD3 region (clone 4-115A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0290
R:Yamada, M.; Maeserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0290
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Cross-references: UNIPARC:UPI000017C1FE
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match

25.0%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 EKY 4
111
Db 1 EKY 3

RESULT 15

S47373
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47373
R:Lehner, P.U.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47373
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116671; EMBL:Z35672; NID:9527489; PIDD:CAA84741.1; PI
C:Keywords: T-cell receptor

Query Match

25.0%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKY 9

111
Db 10 EKY 12

Search completed: June 13, 2006, 03:11:40
Job time : 39 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:02:51 ; Search time 291 Seconds
(without alignments)
41.324 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 937

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	33.8	13	2	Q50038_MYCLE
2	21	30.9	13	1	TEML_RANTE
3	20	29.4	13	2	Q6S4R5_LEICH
4	20	29.4	13	2	Q3LYX0_9INFA
5	19	27.9	13	2	Q93824_CANTRA
6	19	27.9	13	2	Q3KYR7_PHOPO
7	19	27.9	13	2	Q6I129_SRHAB
8	18	26.5	13	2	Q4YMR8_PLABE
9	18	26.5	13	2	Q7M2Z6_SHEEP
10	18	26.5	13	2	Q9TU76_SHEEP
11	18	26.5	13	2	Q86260_KLEPN
12	18	26.5	13	2	Q9RSN5_CLEBO
13	18	26.5	13	2	Q2WDU0_FTICAL
14	17	25.0	13	1	E121_LITRU
15	17	25.0	13	1	H122_LITRU
16	17	25.0	13	1	HDLA_ARCPR
17	17	25.0	13	2	Q96066_HUMAN
18	17	25.0	13	2	Q9UP57_HUMAN
19	17	25.0	13	2	Q8WEJ9_GINBI
20	17	25.0	13	2	Q8WEKO_CYCCI
21	17	25.0	13	2	Q6TMP8_STRCL
22	17	25.0	13	2	Q9QW04_3MURI
23	17	25.0	13	2	P90442_NPVSL
24	16	23.5	13	1	CRTC_BOVIN
25	16	23.5	13	1	DRAM3_LYMST
26	16	23.5	13	1	HSP7D_RAT
27	16	23.5	13	2	Q7SCD5_NEUCR
28	16	23.5	13	2	Q8WXG0_HUMAN
29	16	23.5	13	2	Q9UDE0_HUMAN
30	16	23.5	13	2	Q7MLJ1_SPTOL
31	16	23.5	13	2	Q85HT3_9SPER

32	16	23.5	13	2	Q8WEJ8_GMEGN	Q8WEJ8 gnetum gnet
33	16	23.5	13	2	Q83171_SVIRU	Q83171 cauliflower
34	16	23.5	13	2	Q5EX74_SPHPU	Q5EX74 sphendon p
35	16	23.5	13	2	Q98YJ7_9HIV1	Q98YJ7 human immun
36	15	22.1	13	1	NEUT_CAVPO	P32560 cavia porce
37	15	22.1	13	2	Q2VR70_9PEZI	Q2VR70 cercospora
38	15	22.1	13	2	Q2VR11_9PEZI	Q2VR11 cercospora
39	15	22.1	13	2	Q2VR12_9PEZI	Q2VR12 cercospora
40	15	22.1	13	2	Q2VR13_9PEZI	Q2VR13 cercospora
41	15	22.1	13	2	Q2VR14_9PEZI	Q2VR14 cercospora
42	15	22.1	13	2	Q2VR16_9PEZI	Q2VR16 cercospora
43	15	22.1	13	2	Q35793_YEAST	Q35793 saccharomyc
44	15	22.1	13	2	Q49WC3_9PEZI	Q49WC3 fusio
45	15	22.1	13	2	Q49WC4_9PEZI	Q49WC4 fusio

ALIGNMENTS

```

RESULT 1
Q50038_MYCLE PRELIMINARY; PRT; 13 AA.
AC Q50038;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE U22661.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Robinson K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U15182; AAA62970.1; -; Genomic DNA.
SQ SEQUENCE 13 AA; 1589 MW; C7CCD7E47D025B06 CRC64;

Query Match 33.8%; Score 23; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.3e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKYLGEE 8
   :||| |
Db 6 QEYLGEV 12

RESULT 2
TEML_RANTE STANDARD; PRT; 13 AA.
ID P57104;
AC P57104;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Tempurin-L.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OC Rana.
OX NCBI_TaxID=8407;
OX [1]
RP PROTEIN SEQUENCE.
RP TISSUE=skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,

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RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
-----
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CC
KW Amidation; Amphibian defense peptide; Antibiotic; Antimicrobial;
KM Direct protein sequencing.
FT PEPTIDE 1 13
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1641 MW; 9EBBCB1FAFF7C325 CRC64;
SQ
Query Match 30.9%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEKYLG 6
Db 5 FSKFGL 10

RESULT 3
06S4R5_LEICH PRELIMINARY; PRT; 13 AA.
ID 06S4R5_LEICH
AC 06S4R5;
DC 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Alpha tubulin (Fragment).
OS Leishmania chagasi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=44271;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MHOM/BR/001/1669;
RX PubMed=15886291; DOI=10.1016/j.expara.2005.02.008;
RA Purdy J.E., Doneison J.E., Wilson M.E.;
RT "Leishmania chagasi: The alpha-tubulin intercoding region results in
RT constant levels of mRNA abundance despite protein synthesis inhibition
RT and growth state.";
RL Exp. Parasitol. 110:102-107(2005).
-----
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CC
EMBL: AY46450; AAR8132.1; -; Genomic_DNA.
FT NON_TER 1 1
FT SEQUENCE 13 AA; 1488 MW; 3F361B0689741B18 CRC64;
SQ
Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 4.2e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LGEEYK 11
Db 5 MGEEDVE 11

RESULT 4
Q3LYX0_91NFA PRELIMINARY; PRT; 13 AA.
ID Q3LYX0_91NFA
AC Q3LYX0;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.

```

```

DT 07-FEB-2006, entry version 5.
DE Matrix protein 1 (Fragment).
GN Name=M;
OS Influenza A virus (A/shorebird/Delaware/275/2001 (H9N7)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
CC Influenzavirus A.
OX NCBI_TaxID=342210;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A/shorebird/Delaware/275/2001;
RX PubMed=16081121; DOI=10.1016/j.virol.2005.07.003;
RA Ilyushina N.A., Govorkova E.A., Webster R.G.;
RT "Detection of amantadine-resistant variants among avian influenza
RT viruses isolated in North America and Asia.";
RL Virology 341:102-106(2005).
CC
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CC
EMBL: DQ107506; ABA12424.1; -; mRNA.
FT VIRAL_MATRIX_PROTEIN 1
FT NON_TER 1
FT SEQUENCE 13 AA; 1700 MW; 274716F5CDBFC2C8 CRC64;
SQ
Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.2e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEKYLG 6
Db 1 YOKRMG 6

RESULT 5
093824_CANTR PRELIMINARY; PRT; 13 AA.
ID 093824_CANTR
AC 093824;
DC 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE UDP-galactose-4-epimerase (Fragment).
GN Name=GAL10;
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5482;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PK233;
RA Kanai T., Ueda M., Tanaka A.;
RT "Candida tropicalis promoter region of GAL1 and GAL10 gene.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC
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CC
EMBL: AB019434; BAA34351.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1312 MW; 0B559D6AB18BC720 CRC64;
SQ
Query Match 27.9%; Score 19; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.1e+04;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LGEEYV 10
Db 1 MSDEVI 6

RESULT 6
Q3KYR7_PHOPO PRELIMINARY; PRT; 13 AA.
ID Q3KYR7_PHOPO

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AC 02KX7;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Acyl-protein synthetase (Fragment).
GN Name=luxE;
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ES-4.2; DOI=10.1111/j.1462-2920.2005.00859.x;
RX PubMed=16156737;
RA Aet J.C., Dunlap P.V.;
RT "Phylogenetic resolution and habitat specificity of members of the
RT Photobacterium phosphoreum species group.";
RL Environ. Microbiol. 7:1641-1654(2005).
CC -----
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CC -----
DR EMBL: AY849494; AAX51447.1; -; Genomic_DNA.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1536 MW; 8A763CB6027A1AA CRC64;

Query Match 27.9%; Score 19; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKTU 5
DB 9 EKYI 12

RESULT 7
Q86129_9RHAB PRELIMINARY; PRT; 13 AA.
ID Q86129_9RHAB
AC Q86129;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE NS protein (Fragment).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Dimarhabdovirus supergroup; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=80001959; PubMed=89911; DOI=10.1016/0092-8674(79)90274-5;
RA McGeoch D.J.;
RT "Structure of the gene N: gene NS intergenic junction in the
RT genome of vesicular stomatitis virus.";
RL Cell 17:673-681(1979).
CC -----
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CC -----
DR EMBL: V01210; CAA24522.1; -; Genomic_RNA.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1597 MW; 42B91799503D12C3 CRC64;

Query Match 27.9%; Score 19; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 EYKA 12
DB 9 EYLS 13

RESULT 8
Q4YMR8_PLABE

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ID Q4YMR8_PLABE PRELIMINARY; PRT; 13 AA.
AC Q4YMR8;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=PB40005.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Palm A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R. III,
RA Katatos F.C., Janse C.V., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: CA01003487; CA100692.1; -; Genomic_DNA.
RX Hypothetical protein.
SQ SEQUENCE 13 AA; 1620 MW; F4F283BE31621051 CRC64;

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLGEYKAV 13
DB 4 HLHTEYLHSV 13

RESULT 9
Q7M226_SHEEP PRELIMINARY; PRT; 13 AA.
ID Q7M226_SHEEP
AC Q7M226;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Enkephalin precursor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=84128045; PubMed=6546517;
RA Micranovic R., Ray P., Krugel W., Lewis R.V.;
RT "Purification and sequence of an opioid peptide derived from ovine
RT piroenkephalin.";
RL Biochem. Biophys. Res. Commun. 118:299-303(1984).
CC -----
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CC -----
DR PIR: A32734; A32734.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1371 MW; 23A7133EA7DF0338 CRC64;

Query Match 26.5%; Score 18; DB 2; Length 13;

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Best Local Similarity 60.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LGEY 9
|:|
Db 5 LGRY 9

RESULT 10
Q9TU76 SHEEP PRELIMINARY; PRT; 13 AA.
AC Q9TU76;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Interleukin 1 alpha (Fragment).
GN Name=IL1A;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99397042; Pubmed=10467711;
RA Maddox J.F., Hawken R.J., Matthew P., Davies K.P.;
RT "Single strand conformational polymorphisms (SSCPs) in the ovine IL1A
and IL6 genes";
RL Anim. Genet. 30:317-318(1999).
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CC EMBL; AF117652; AAD5050.1; -, Genomic_DNA.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1520 MW; C26BC6198305DB5D CRC64;

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YLGE 8
|:|
Db 7 YVSE 11

RESULT 11
O86260 KLEPN PRELIMINARY; PRT; 13 AA.
AC O86260;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Trx protein (Fragment).
GN Name=trxB;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MSA1;
RA Albrecht C., Kleiner D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
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CC EMBL; Y17587; CAA6799.1; -, Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 13 AA; 1425 MW; 890C8715ECD2287A CRC64;

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ERYL 5
|:|
Db 2 ERYL 5

RESULT 12
Q9RSN5 CLOBO PRELIMINARY; PRT; 13 AA.
AC Q9RSN5;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Neurotoxin type B HN+ 35 kDa SUBUNIT=BAND 3B (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92143938; Pubmed=1781887;
RA Somers E., Dasgupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
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CC PIR; G44644; G44644.
FT NON TER 13
SQ SEQUENCE 13 AA; 1539 MW; 00DB6E78247E2054 CRC64;

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YERYLGEYV 10
|:|:|
Db 4 YQNIINDKIV 13

RESULT 13
Q2WDU0 FICAL PRELIMINARY; PRT; 13 AA.
AC Q2WDU0;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromo-helicase-DNA-binding on the Z chromosome (Fragment).
GN Name=chdz;
OS Piceula albicollis (collared flycatcher).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Picedula.
OX NCBI_TaxID=59894;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IC2;
RX Pubmed=15956661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
RT Chromosome and Autosomes in Two Picedula Flycatcher Species.";
RL Genetics 171:1661-1873(2005).
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CC EMBL; AJ869811; CAI35564.1; -, Genomic_DNA.
GO; GO:0003677; F:DNA binding; IEA.

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DR  GO: 0004386; F:helix activity; IEA.
KM  DNA-binding; Helicase.
FT  NON_TER 1
SQ  SEQUENCE 13 AA; 1703 MW; 5FEBFP28DB81B53 CRC64;

Query Match      26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  8 EYVK 11
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Db  3 EYVK 6

RESULT 14
E121 LITRU STANDARD; PRT; 13 AA.
ID  E121 LITRU
AC  P82057;
DT  23-JAN-2002, integrated into UniProtKB/Swiss-Prot.
DT  01-MAY-2000, sequence version 1.
DE  07-FEB-2006, entry version 22.
DE  Electrin-2.1.
OC  Litoria rubella (Desert tree frog).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC  Pelodyadinae; Litoria.
OX  NCBI_TaxID=104895;
RN  [1]
RP  PROTEIN SEQUENCE.
RC  Tissue=Skin secretion;
RA  Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT  "Peptides from the skin glands of the Australian buzzing tree frog
RT  Litoria electrica. Comparison with the skin peptides from Litoria
RT  rubella."
RL  Aust. J. Chem. 52:639-645(1999).
CC  -!- SUBCELLULAR LOCATION: Secreted protein.
CC  -!- TISSUE SPECIFICITY: Expressed by the skin glands.
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KM  Amidation; Amphibian defense peptide; Direct protein sequencing.
FT  PEPTIDE 1 13
    /FTID=PRO_0000043792.
FT  MOD_RES 13 13
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SQ  SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match      25.0%; Score 17; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  7 EYVK 11
    |||
Db  3 EYVK 7

RESULT 15
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ID  E122 LITRU
AC  P82058;
DT  23-JAN-2002, integrated into UniProtKB/Swiss-Prot.
DT  01-MAY-2000, sequence version 1.
DE  07-FEB-2006, entry version 22.
DE  Electrin-2.2.
OC  Litoria rubella (Desert tree frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC  Pelodyadinae; Litoria.
OX  NCBI_TaxID=104895;
RN  [1]
RP  PROTEIN SEQUENCE.
RC  Tissue=Skin secretion;

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RA  Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT  "Peptides from the skin glands of the Australian buzzing tree frog
RT  Litoria electrica. Comparison with the skin peptides from Litoria
RT  rubella."
RL  Aust. J. Chem. 52:639-645(1999).
CC  -!- SUBCELLULAR LOCATION: Secreted protein.
CC  -!- TISSUE SPECIFICITY: Expressed by the skin glands.
CC  -----
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CC  -----
KM  Amidation; Amphibian defense peptide; Direct protein sequencing.
FT  PEPTIDE 1 13
    /FTID=PRO_0000043793.
FT  MOD_RES 13 13
    Proline amide.
SQ  SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match      25.0%; Score 17; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  7 EYVK 11
    |||
Db  3 EYVK 7

Search completed: June 13, 2006, 03:10:57
Job time : 293 secs

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OM protein - protein search, using sw model

Run on: June 13, 2006, 03:11:12 ; Search time 50 Seconds
(without alignments)
22,758 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 8406

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /EMC_Celerra_SIDS3/prodata/2/1aa/6 COMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/1aa/7 COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/H COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCTUS COMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/1aa/RE COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfilltest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	35.3	13	2	US-09-534-717-494 Sequence 484, App
2	23	33.8	13	1	US-08-465-325-135 Sequence 135, App
3	23	33.8	13	2	US-09-115-737-135 Sequence 135, App
4	23	33.8	13	2	US-09-060-450-8 Sequence 8, Appl
5	23	33.8	13	2	US-09-759-484-7 Sequence 7, Appl
6	23	33.8	13	2	US-10-146-305-14 Sequence 14, Appl
7	23	33.8	13	7	5244657-2 Patent No. 5244657
8	22	32.4	13	1	US-08-460-190-40 Sequence 40, Appl
9	22	32.4	13	1	US-08-596-3878-22 Sequence 22, Appl
10	22	32.4	13	1	US-08-488-379-40 Sequence 40, Appl
11	22	32.4	13	2	US-09-171-945-33 Sequence 33, Appl
12	22	32.4	13	2	US-09-067-615-22 Sequence 22, Appl
13	22	32.4	13	2	US-09-374-671A-108 Sequence 108, App
14	22	32.4	13	2	US-08-475-399A-40 Sequence 40, Appl
15	22	32.4	13	2	US-09-574-749B-45 Sequence 45, Appl
16	22	32.4	13	2	US-08-077-255A-40 Sequence 40, Appl
17	22	32.4	13	2	US-08-908-469-84 Sequence 84, Appl
18	22	32.4	13	2	US-09-910-059-33 Sequence 33, Appl
19	22	32.4	13	3	US-10-196-107A-108 Sequence 108, App
20	22	32.4	13	5	PCT-US93-05701-14 Sequence 14, Appl
21	22	32.4	13	5	PCT-US93-07545-40 Sequence 40, Appl
22	22	32.4	13	5	PCT-US95-09816A-22 Sequence 22, Appl
23	21	30.9	13	1	US-08-594-447-6 Sequence 6, Appl
24	21	30.9	13	1	US-08-541-964-5 Sequence 5, Appl
25	21	30.9	13	1	US-08-787-547-42 Sequence 42, Appl
26	21	30.9	13	1	US-08-665-647-20 Sequence 20, Appl

27	21	30.9	13	2	US-08-374-077C-47 Sequence 47, Appl
28	21	30.9	13	2	US-08-374-077C-48 Sequence 48, Appl
29	21	30.9	13	2	US-08-895-590-89 Sequence 89, Appl
30	21	30.9	13	2	US-08-895-590-90 Sequence 90, Appl
31	21	30.9	13	2	US-09-319-730-10 Sequence 10, Appl
32	21	30.9	13	2	US-09-539-879A-47 Sequence 47, Appl
33	21	30.9	13	2	US-09-539-879A-48 Sequence 48, Appl
34	21	30.9	13	2	US-09-379-297-4 Sequence 4, Appl
35	21	30.9	13	2	US-09-756-247-14 Sequence 14, Appl
36	21	30.9	13	2	US-09-756-247-35 Sequence 35, Appl
37	21	30.9	13	2	US-09-936-885A-26 Sequence 26, Appl
38	21	30.9	13	2	US-09-820-053A-78 Sequence 78, Appl
39	21	30.9	13	5	PCT-US94-10257A-26 Sequence 26, Appl
40	20	29.4	13	1	US-07-632-027-5 Sequence 5, Appl
41	20	29.4	13	1	US-07-932-455A-17 Sequence 17, Appl
42	20	29.4	13	1	US-08-766-725A-17 Sequence 17, Appl
43	20	29.4	13	1	US-08-430-521-9 Sequence 9, Appl
44	20	29.4	13	1	US-08-844-031-36 Sequence 36, Appl
45	20	29.4	13	2	US-09-126-420A-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-534-717-494
; Sequence 494, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CD
; CURRENT APPLICATION NUMBER: US/09/534, 717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 494
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-494

Query Match 35.3%; Score 24; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LGERYVK 11
Db 7 IGSNYVK 13

RESULT 2
US-08-465-325-135
; Sequence 135, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 510 Campus Drive
; TITLE OF INVENTION: Biologically Active Peptides Having
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-325-135

Query Match 33.8%; Score 23; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KYLGEYVK 11
| | | | |
1 KKFQKKFKV 9

RESULT 3
US-09-115-737-135
Sequence 135, Application US/09115737
Patent No. 634845
GENERAL INFORMATION:
APPLICANT: U. Prasad Karti
Michael McLane
Taffy J. Williams
TITLE OF INVENTION: Biologically Active Peptides With Reduced
Toxicity in Animals and a Method for Preparing Same
NUMBER OF SEQUENCES: 156
CORRESPONDENCE ADDRESSES:
ADDRESSES: Finnegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,737
FILING DATE: 15-JUL-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,330
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
APPLICATION NUMBER: 07/891,201

FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-06000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-09-115-737-135

Query Match 33.8%; Score 23; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KYLGEYVK 11
| | | | |
1 KKFQKKFKV 9

RESULT 4
US-09-060-450-8
Sequence 8, Application US/09060450
Patent No. 6669945
GENERAL INFORMATION:
APPLICANT: Nardin, Elizabeth
MORENO, Alberto
TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
FILE REFERENCE: 5986/1B615-US1
CURRENT APPLICATION NUMBER: US/09/060,450
CURRENT FILING DATE: 1998-01-21
EARLIER APPLICATION NUMBER: 60/033,916
EARLIER FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: UD4 peptide containing DR 4 allele specific binding
OTHER INFORMATION: motifs for use as indicator peptide.
US-09-060-450-8

Query Match 33.8%; Score 23; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 YEKYGEYVKA 12
| | | | |
1 YKFKVKNITLKA 12

RESULT 5
US-09-759-484-7
Sequence 7, Application US/09759484
Patent No. 6838579
GENERAL INFORMATION:
APPLICANT: William Harvey Research Limited
TITLE OF INVENTION: Anti-inflammatory compounds
FILE REFERENCE: P019602WO
CURRENT APPLICATION NUMBER: US/09/759,484
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7

LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-759-484-7

Query Match 33.8%; Score 23; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 EBYKAV 13
DB 7 QBYVQTV 13

RESULT 6
US-10-146-305-14
Sequence 14, Application US/10146305
Patent No. 6939956
GENERAL INFORMATION:
APPLICANT: YUHAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
FILE REFERENCE: OVI17440
CURRENT APPLICATION NUMBER: US/10/146,305
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Kopatencin 1.71
SEQ ID NO 14
LENGTH: 13
TYPE: PRT
ORGANISM: Escherichia coli
US-10-146-305-14

Query Match 33.8%; Score 23; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YLGEY 9
DB 4 FLGEGY 9

RESULT 7
5244657-2
Patent No. 5244657
APPLICANT: KLIEN, MICHEL A.;BOUX, HEATHER A.;COCKLE,
STEPHEN A.;LOOSMORE, SHEENA M.;ZEALEY, GAVIN R.
TITLE OF INVENTION: GENETIC DETOXIFICATION OF PERTUSSIS
TOXIN
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/589,423
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 275,376
FILING DATE: 23-NOV-1988
SEQ ID NO: 2
LENGTH: 13
5244657-2

Query Match 33.8%; Score 23; DB 7; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYL 5
DB 8 YESYL 12

RESULT 8
US-08-480-190-40
Sequence 40, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:

APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-40

Query Match 32.4%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 EBYKAV 13
DB 4 EBYLKKI 10

RESULT 9
US-08-596-387B-22
Sequence 22, Application US/08596387B
Patent No. 5869270
GENERAL INFORMATION:

APPLICANT: Rhode, Peter R.
APPLICANT: Jiao, Jin-An
APPLICANT: Burkhart, Martin
APPLICANT: Wong, Hing
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dade International, Inc.

```

; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,387B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US-08-596-387B-22

Query Match      32.4%; Score 22; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KYLG 6
Db      5 KYLG 8

RESULT 10
US-08-488-379-40
; Sequence 40, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vismali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-40

Query Match      32.4%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      7 EBYKAV 13
Db      4 EBYLKKI 10

RESULT 11
US-09-171-945-33
; Sequence 33, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-33

Query Match      32.4%; Score 22; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 YEKYLGEEY 9
Db      5 YAGYLANDY 13

RESULT 12
US-09-067-615-22
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; Sequence 22, Application US/09067615
; Patent No. 6309645
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MAC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,387
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-C1P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US-09-067-615-22

Query Match      32.4%; Score 22; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 KYLG 6
Db 5 KYLG 8

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RESULT 13
; Sequence 108, Application US/09374671A
; Patent No. 6489118
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; APPLICANT: Konieczny, Andrzej
; APPLICANT: Bizindakas, Christine B.
; APPLICANT: Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amy E. Mandragouras
; STREET: 28 State Street
```

```
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/374,671A
; FILING DATE: 16-Aug-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,549
; FILING DATE: 1993-NOV-22
; APPLICATION NUMBER: US 07/999,712
; FILING DATE: 1992-DEC-31
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiorgio, Jeanne M.
; REGISTRATION NUMBER: 41,710
; REFERENCE/DOCKET NUMBER: IMI-026C2CNCPPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
; US-09-374-671A-108
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Query Match      32.4%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 6 GEEYKAV 13
Db 1 GKWYLKAM 8

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RESULT 14
; Sequence 40, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
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FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-40

Query Match 32.4%; Score 22; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 EBYKAV 13
|:|:|:
Db 4 EGYLKKI 10

RESULT 15
US-09-574-749B-45
Sequence 45, Application US/09574749B
Patent No. 6548299
GENERAL INFORMATION:
APPLICANT: ROSENZWEIG, Michael
APPLICANT: PYKETT, Mark J.
APPLICANT: SCADDEN, David T.
APPLICANT: POZNANSKY, Mark C.
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
TITLE OF INVENTION: DEVICES
FILE REFERENCE: C1005/7012/KA/ERG
CURRENT APPLICATION NUMBER: US/09/574,749B
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/107,972
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/US99/26795
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/524,749
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 45
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Influenza source
US-09-574-749B-45

Query Match 32.4%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 EBYKAV 11
|:|:|:
Db 1 EBYKAV 5

Search completed: June 13, 2006, 03:12:35
Job time: 51 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2006, 03:23:17 ; Search time 181 Seconds
(without alignments)
33.270 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 20666

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
1: /EMC_Celerra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	13	4	US-10-612-162-4
2	30	44.1	13	5	US-10-823-253-3
3	30	44.1	13	5	US-10-823-810-3
4	30	44.1	13	6	US-11-105-268-3
5	26	38.2	13	4	US-10-280-139-11
6	25	36.8	13	5	US-10-823-253-12
7	25	36.8	13	5	US-10-930-300-101
8	25	36.8	13	5	US-10-930-300-108
9	25	36.8	13	5	US-10-930-300-113
10	25	36.8	13	5	US-10-823-810-12
11	25	36.8	13	5	US-10-946-647-889
12	25	36.8	13	6	US-11-105-268-12
13	25	36.8	13	6	US-11-152-974A-302
14	25	36.8	13	6	US-11-153-143A-302
15	24	35.3	13	4	US-10-080-880-18
16	24	35.3	13	4	US-10-327-598-569
17	24	35.3	13	5	US-10-884-830-494
18	24	35.3	13	5	US-10-996-316-189
19	24	35.3	13	6	US-10-948-707-784
20	24	35.3	13	6	US-11-171-567-189
21	23	33.8	13	3	US-09-759-484-7
22	23	33.8	13	4	US-10-146-305-14
23	23	33.8	13	4	US-10-001-934-7
24	23	33.8	13	4	US-10-056-884-16
25	23	33.8	13	4	US-10-275-046-51
26	23	33.8	13	4	US-10-432-422-130
27	23	33.8	13	4	US-10-469-837-11

28	23	33.8	13	4	US-10-469-837-12	Sequence 12, Appl
29	23	33.8	13	4	US-10-469-837-13	Sequence 13, Appl
30	23	33.8	13	4	US-10-469-837-14	Sequence 14, Appl
31	23	33.8	13	5	US-10-834-666-44	Sequence 44, Appl
32	23	33.8	13	5	US-10-930-300-98	Sequence 98, Appl
33	23	33.8	13	5	US-10-930-300-100	Sequence 100, Appl
34	23	33.8	13	5	US-10-930-300-102	Sequence 102, Appl
35	23	33.8	13	5	US-10-930-300-105	Sequence 105, Appl
36	23	33.8	13	5	US-10-930-300-107	Sequence 107, Appl
37	23	33.8	13	5	US-10-930-300-109	Sequence 109, Appl
38	23	33.8	13	5	US-10-930-300-112	Sequence 112, Appl
39	23	33.8	13	5	US-10-470-048B-603	Sequence 603, Appl
40	23	33.8	13	5	US-10-286-313-1	Sequence 1, Appl
41	23	33.8	13	5	US-10-958-216-716	Sequence 716, Appl
42	23	33.8	13	5	US-10-948-707-745	Sequence 745, Appl
43	23	33.8	13	5	US-10-948-707-911	Sequence 911, Appl
44	23	33.8	13	5	US-10-948-707-1360	Sequence 1360, Appl
45	23	33.8	13	5	US-10-716-189-8	Sequence 8, Appl

ALIGNMENTS

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RESULT 1
US-10-612-162-4
; Sequence 4, Application US/10612162
; Publication No. US2004001415A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-612-162-4

Query Match      100.0%; Score 68; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      1 YEKYLGEYVKAV 13

RESULT 2
US-10-823-253-3
; Sequence 3, Application US/10823253
; Publication No. US20050002934A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Jennifer
; TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10271-112-999
; CURRENT APPLICATION NUMBER: US/10/823,253
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,259
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/477,797
; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 13
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-253-3

Query Match 44.1%; Score 30; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
| : |||
Db 3 YGSDYVK 10

RESULT 3
US-10-823-810-3
Sequence 3, Application US/10823810
Publication No. US20050147607A1
GENERAL INFORMATION:

APPLICANT: Reed, Jennifer
TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
FILE REFERENCE: 10271-113-999
CURRENT APPLICATION NUMBER: US/10/823,810
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 60/462,307
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 60/477,801
PRIOR FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-810-3

Query Match 44.1%; Score 30; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
| : |||
Db 3 YGSDYVK 10

RESULT 4
US-11-105-268-3
Sequence 3, Application US/1105268
Publication No. US20050260204A1
GENERAL INFORMATION:

APPLICANT: Allan, Christian
TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
FILE REFERENCE: 10271-126-999
CURRENT APPLICATION NUMBER: US/11/105,268
CURRENT FILING DATE: 2005-04-12
PRIOR APPLICATION NUMBER: 60/561,845
PRIOR FILING DATE: 2004-04-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-11-105-268-3

Query Match 44.1%; Score 30; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
| : |||
Db 3 YGSDYVK 10

RESULT 5
US-10-280-139-11

Sequence 11, Application US/10280139
Publication No. US20040081963A1
GENERAL INFORMATION:
APPLICANT: Wang, Yan
APPLICANT: Mj Bioworks Incorporated
TITLE OF INVENTION: Improved Sae7-Polymerase Conjugate Proteins
FILE REFERENCE: 020130-001200US
CURRENT APPLICATION NUMBER: US/10/280,139
CURRENT FILING DATE: 2002-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sae7d and Sae7e
US-10-280-139-11

Query Match 38.2%; Score 26; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KYLGE 8
| : |||
Db 4 KYGGE 9

RESULT 6
US-10-823-253-12
Sequence 12, Application US/10823253
Publication No. US2005002934A1
GENERAL INFORMATION:
APPLICANT: Reed, Jennifer
TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF
FILE REFERENCE: 10271-112-999
CURRENT APPLICATION NUMBER: US/10/823,253
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 60/462,259
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 60/477,797
PRIOR FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-253-12

Query Match 36.8%; Score 25; DB 5; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
| : |||
Db 3 YGSDYVK 10

RESULT 7
US-10-930-300-101
Sequence 101, Application US/10930300
Publication No. US20050014138A1
GENERAL INFORMATION:
APPLICANT: Rath, Matthias
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT

STREET: 280 Colorado Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MS WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-AUG-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,248
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
REGISTRATION NUMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-322-7371
TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-930-300-101
Query Match 36.8%; Score 25; DB 5; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 YEKYLGEYVK 11
Db 2 YSKYLDNRRRK 12
RESULT 8
US-10-930-300-108
Sequence 108, Application US/10930300
Publication No. US20050014138A1
GENERAL INFORMATION:
APPLICANT: Rath, Matthias
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
OLIGOPEPTIDES
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 Colorado Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MS WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-AUG-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,248
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
REGISTRATION NUMBER: 37000

REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-322-7371
TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-930-300-108
Query Match 36.8%; Score 25; DB 5; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 YEKYLGEYVK 11
Db 2 YSKYLDNRRRK 12
RESULT 9
US-10-930-300-113
Sequence 113, Application US/10930300
Publication No. US20050014138A1
GENERAL INFORMATION:
APPLICANT: Rath, Matthias
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
OLIGOPEPTIDES
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 Colorado Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MS WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-AUG-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,248
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
REGISTRATION NUMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-322-7371
TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-930-300-113
Query Match 36.8%; Score 25; DB 5; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 YEKYLGEYVK 11
Db 2 YSKYLDNRRRK 12

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RESULT 10
US-10-823-810-12
; Sequence 12, Application US/10823810
; Publication No. US20050147607A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Jennifer
; TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
; FILE REFERENCE: 10271-113-999
; CURRENT APPLICATION NUMBER: US/10/823, 810
; PRIOR FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,307
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/477,801
; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-810-12

Query Match      36.8%; Score 25; DB 5; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 YLGEYVKA 12
      | | | | |
Db      1 YASPEYVQA 9

RESULT 11
US-10-946-647-889
; Sequence 889, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293, 00340101
; CURRENT APPLICATION NUMBER: US/10/946, 647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 889
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-946-647-889

Query Match      36.8%; Score 25; DB 5; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      4 YLGEYVKA 12
      | | | | |
Db      1 YASPEYVQA 9

RESULT 12
US-11-105-268-12
; Sequence 12, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allian, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105, 268
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; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-12

Query Match      36.8%; Score 25; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 YLGEYVKA 11
      | | | | |
Db      3 YYGSDHVK 10

RESULT 13
US-11-152-974A-302
; Sequence 302, Application US/11152974A
; Publication No. US20060051395A1
; GENERAL INFORMATION:
; APPLICANT: Wayne F. Beyer, Jr.
; APPLICANT: Robin Hyde-Deruysscher
; APPLICANT: Paul T. Hamilton
; APPLICANT: Ray Edward Benson
; TITLE OF INVENTION: IFMBs to Promote the Specific Attachment of Target Analytes to the
; FILE REFERENCE: APO06
; CURRENT APPLICATION NUMBER: US/11/152, 974A
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/580, 019
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/651,338
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/651,747
; PRIOR FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 558
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated from phage display libraries
US-11-152-974A-302

Query Match      36.8%; Score 25; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YEKYIG 6
      | | | | |
Db      7 YDKYSG 12

RESULT 14
US-11-153-143A-302
; Sequence 302, Application US/11153143A
; Publication No. US20060051396A1
; GENERAL INFORMATION:
; APPLICANT: Paul T. Hamilton
; APPLICANT: Mark W. Grinstaff
; APPLICANT: Daniel J. Kenan
; APPLICANT: Dale J. Christensen
; TITLE OF INVENTION: Biofunctional Coatings
; FILE REFERENCE: APO05
; CURRENT APPLICATION NUMBER: US/11/153, 143A
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/580, 019
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; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/651,338
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/651,747
; PRIOR FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 558
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: isolated from phage display libraries
US-11-153-143A-302

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Query Match          36.8%; Score 25; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 YEKYLG 6
        |||||
Db       7 YDKYSG 12

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RESULT 15
US-10-080-980-18
; Sequence 18, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-080-980-18

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Query Match          35.3%; Score 24; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      2 EKYLGEEYVK 11
        |||||
Db       3 ERYTSRYLTK 12

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 Job time : 182 secs

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OM protein - protein search, using ew model

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(without alignments)
4.442 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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3: /EMC_Ceiera_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep: *
4: /EMC_Ceiera_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep: *
5: /EMC_Ceiera_SIDS3/ptodata/1/pubpaa/US09_PCT_NEW_PUB pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	32.4	13	6	US-10-497-088-5
2	22	32.4	13	7	US-11-259-950-33
3	21	30.9	13	7	US-11-264-509A-132
4	20	29.4	13	6	US-10-538-066-38
5	20	29.4	13	6	US-10-538-066-41
6	20	29.4	13	7	US-11-038-754-18
7	19	27.9	13	6	US-10-614-959-13
8	19	27.9	13	7	US-11-264-509A-94
9	19	27.9	13	7	US-11-313-356-20
10	18	26.5	13	6	US-10-538-066-35
11	17	25.0	13	6	US-10-538-066-32
12	17	25.0	13	6	US-10-538-066-651
13	17	25.0	13	7	US-11-264-509A-128
14	17	25.0	13	7	US-11-264-509A-138
15	17	25.0	13	7	US-11-261-429-21
16	16	23.5	13	6	US-10-538-066-36
17	16	23.5	13	6	US-10-538-066-39
18	16	23.5	13	7	US-11-257-498-46
19	16	23.5	13	7	US-11-257-498-47
20	16	23.5	13	7	US-11-054-072-5004
21	16	23.5	13	7	US-11-054-072-5005
22	16	23.5	13	7	US-11-054-072-5006
23	16	23.5	13	7	US-11-054-072-5007
24	16	23.5	13	7	US-11-054-072-5008
25	16	23.5	13	7	US-11-054-072-5009

26	16	23.5	13	7	US-11-054-072-5010	Sequence 5010, Ap
27	16	23.5	13	7	US-11-054-072-5011	Sequence 5011, Ap
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30	16	23.5	13	7	US-11-054-072-5014	Sequence 5014, Ap
31	16	23.5	13	7	US-11-054-072-5015	Sequence 5015, Ap
32	16	23.5	13	7	US-11-054-072-5016	Sequence 5016, Ap
33	16	23.5	13	7	US-11-054-072-5017	Sequence 5017, Ap
34	16	23.5	13	7	US-11-054-072-5018	Sequence 5018, Ap
35	16	23.5	13	7	US-11-054-072-5019	Sequence 5019, Ap
36	16	23.5	13	7	US-11-054-072-5020	Sequence 5020, Ap
37	16	23.5	13	7	US-11-054-072-5021	Sequence 5021, Ap
38	16	23.5	13	7	US-11-054-072-5022	Sequence 5022, Ap
39	16	23.5	13	7	US-11-054-072-5023	Sequence 5023, Ap
40	16	23.5	13	7	US-11-054-072-5024	Sequence 5024, Ap
41	16	23.5	13	7	US-11-054-072-5025	Sequence 5025, Ap
42	16	23.5	13	7	US-11-054-072-5026	Sequence 5026, Ap
43	16	23.5	13	7	US-11-054-072-5027	Sequence 5027, Ap
44	16	23.5	13	7	US-11-233-532-2	Sequence 2, Appl
45	16	23.5	13	7	US-11-264-509A-81	Sequence 81, Appl

ALIGNMENTS

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RESULT 1
US-10-497-088-5
; Sequence 5, Application US/10497088
; Publication No. US20060088520A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Gerneraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Leekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGF-1.DR13 specific peptide
US-10-497-088-5
Query Match 33.4%; Score 22; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 3 KYLGEYKAV 12
Db 3 KYRAEPYKKA 12
RESULT 2
US-11-259-950-33
; Sequence 33, Application US/11259950
; Publication No. US20060088524A1
; GENERAL INFORMATION:
; APPLICANT: Morrissey, James
; APPLICANT: Pureza, Vincent
```

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; APPLICANT: Sligar, Stephen G.
; TITLE OF INVENTION: Tissue Factor Compositions and Methods
; FILE REFERENCE: 46-04
; CURRENT APPLICATION NUMBER: US/11/259,950
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US 60/622,737
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: US 60/536,281
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US 10/465,789
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 11/033,489
; PRIOR FILING DATE: 2005-01-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Helix 10.5
US-11-259-950-33
```

```

Query Match      32.4%; Score 22; DB 7; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 EBYVK 11
      |||
      4 EBYTK 8
```

```

RESULT 3
US-11-264-509A-132
; Sequence 132, Application US/11264509A
; Publication No. US20060100148A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Rong
; APPLICANT: Zhang, Rumin
; APPLICANT: Kong, Rong
; TITLE OF INVENTION: PEPTIDE VIRAL ENTRY PEPTIDES
; FILE REFERENCE: JB062270S01
; CURRENT APPLICATION NUMBER: US/11/264,509A
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/624,204
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV peptide
US-11-264-509A-132
```

```

Query Match      30.9%; Score 21; DB 7; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 EYVK 11
      |||
      5 EYVK 8
```

```

RESULT 4
US-10-538-066-38
; Sequence 38, Application US/10538066
; Publication No. US20060094649A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PADRE Peptide
US-10-538-066-38
```

```

Query Match      29.4%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3 KYLGEYVKA 12
      |||
      2 KYVAHTLKA 11
```

```

RESULT 5
US-10-538-066-41
; Sequence 41, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PADRE Peptide
US-10-538-066-41
```

```

Query Match      29.4%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3 KYLGEYVKA 12
      |||
      2 KYVAHTLKA 11
```

```

RESULT 6
US-11-038-754-18
; Sequence 18, Application US/11038754
; Publication No. US20060115855A1
; GENERAL INFORMATION:
; APPLICANT: Goldkornf, Ira L.
; APPLICANT: Sheta, Essam A.
; APPLICANT: Appel, Stanley H.
; APPLICANT: Simpson, Ericka P.
; APPLICANT: Yen, Albert A.
; TITLE OF INVENTION: AN FK506-BINDING PROTEIN 7 RELATED PROTEIN AS A BIOMARKER FOR
; FILE REFERENCE: PROT-P0012US
```

```

; CURRENT APPLICATION NUMBER: US/11/038,754
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: US 60/632,216
; PRIOR FILING DATE: 2004-12-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-038-754-18

Query Match      29.4%; Score 20; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4 YLGEYVK 11
Db      6 YLQREFEK 13

RESULT 7
US-10-614-959-13
; Sequence 13, Application US/10614959
; Publication No. US20060088534A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camella W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/10/614,959
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/383,667
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/098,233
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/122,767
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-614-959-13

Query Match      27.9%; Score 19; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 LGEYV 10
Db      7 IGNNYV 12

RESULT 8
US-11-264-509A-94
; Sequence 94, Application US/11264509A
; Publication No. US20060100148A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Rong
; APPLICANT: Zhang, Rumin
; APPLICANT: Zhang, Rong
; TITLE OF INVENTION: PEPTIDE VIRAL ENTRY PEPTIDES
; FILE REFERENCE: JB06227US01
; CURRENT APPLICATION NUMBER: US/11/264,509A
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/624,204
; PRIOR FILING DATE: 2004-11-02
```

```

; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV peptide
US-11-264-509A-94

Query Match      27.9%; Score 19; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 EYKAV 13
Db      5 EYVAL 10

RESULT 9
US-11-313-356-20
; Sequence 20, Application US/11313356
; Publication No. US20060105379A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shujian
; APPLICANT: Chen, Jian
; APPLICANT: Feder, John
; APPLICANT: Lee, Liana
; APPLICANT: Krystek, Stanley
; TITLE OF INVENTION: POLYUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY EXPRESSED
; TITLE OF INVENTION: IN THE TESTIS, MMP-29
; FILE REFERENCE: D0141DIV
; CURRENT APPLICATION NUMBER: US/11/313,356
; CURRENT FILING DATE: 2005-12-21
; PRIOR APPLICATION NUMBER: US 60/286,764
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-313-356-20

Query Match      27.9%; Score 19; DB 7; Length 13;
Best Local Similarity 25.0%; Pred. No. 9.2e+02;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      2 EKYGEY 9
Db      2 KKPISKX 9

RESULT 10
US-10-538-066-35
; Sequence 35, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
```

OTHER INFORMATION: PADRE Peptide
US-10-538-066-35

Query Match 26.5%; Score 18; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1,4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KYLGEYVKA 12
||: ||
Db 2 KYVAAYTLKA 11

RESULT 11

US-10-538-066-32
; Sequence 32, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PADRE Peptide
US-10-538-066-32

Query Match 25.0%; Score 17; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KYLGEYVKA 12
||: ||
Db 2 KYVAAYTLKA 11

RESULT 12

US-10-538-066-651
; Sequence 651, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 651
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-651

Query Match 25.0%; Score 17; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 EYVKAV 13
||: ||
Db 2 EYVLQV 7

RESULT 13
US-11-264-509A-128

; Sequence 128, Application US/11264509A
; Publication No. US20060100148A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Rong
; APPLICANT: Zhang, Rumin
; APPLICANT: Kong, Rong
; TITLE OF INVENTION: PEPTIDE VIRAL ENTRY PEPTIDES
; FILE REFERENCE: JB06227US01
; CURRENT APPLICATION NUMBER: US/11/264,509A
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/624,204
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV peptide
US-11-264-509A-128

Query Match 25.0%; Score 17; DB 7; Length 13;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 EYVY 10
||: ||
Db 4 KEYV 7

RESULT 14

US-11-264-509A-138
; Sequence 138, Application US/11264509A
; Publication No. US20060100148A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Rong
; APPLICANT: Zhang, Rumin
; APPLICANT: Kong, Rong
; TITLE OF INVENTION: PEPTIDE VIRAL ENTRY PEPTIDES
; FILE REFERENCE: JB06227US01
; CURRENT APPLICATION NUMBER: US/11/264,509A
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/624,204
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV peptide
US-11-264-509A-138

Query Match 25.0%; Score 17; DB 7; Length 13;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYL 5
||: ||
Db 4 FEVYL 8

RESULT 15

US-11-261-429-21
; Sequence 21, Application US/11261429
; Publication No. US20060115899A1
; GENERAL INFORMATION:
; APPLICANT: Buckner, Jane H.

; APPLICANT: Walker, Mindi R.
; TITLE OF INVENTION: METHODS OF GENERATING ANTIGEN-SPECIFIC CD4+CD25+ REGULATORY T
; FILE OF INVENTION: CELLS, COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: BRIVM-1-26413
; CURRENT APPLICATION NUMBER: US/11/261,429
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US 60/623,380
; PRIOR FILING DATE: 2004-10-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-261-429-21

Query Match 25.0%; Score 17; DB 7; Length 13;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 3 KYLG 6
|:|
Db 5 KWLG 8

Search completed: June 13, 2006, 03:35:20
Job time : 38 secs

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